



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 1653

TO: Rosanne Kosson  
Art Unit: 1653  
Location: REM-3B84&3C18  
Serial Number: 09/856723

Tuesday, May 23, 2006

From: Beverly Shears  
Location: Biotech-Chem Library  
REM 1A54  
Phone: 571-272-2528  
[beverly.shears@uspto.gov](mailto:beverly.shears@uspto.gov)

### Search Notes

Your queries have completed processing. You may access an electronic version via eDAN (SCORE) and /or <http://es/ScoreAccessWeb>. If the result files have been separated into two (2) or more versions, you may view additional files via the select "View version list for this application" link.

#### Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

#### Published Applications Database - November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions .rnpbm (Published\_Applications\_NA\_Main) and .rnpbn (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published\_Applications\_AA\_Main) and .rapbn (Published\_Applications\_AA\_New).



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190532

From: Kosson, Rosanne  
 Sent: Thursday, May 18, 2006 3:55 PM  
 To: STIC-Biotech/ChemLib  
 Subject: request for sequence search- 09/856,723- REGULATORY PROTEIN PKE#83 FROM HUMAN KERATINOCTYES

Please search SEQ ID NO: 8 for me in the commercial and interference databases. This is a protein of 1076 amino acids.  
 My mailbox is in 3C70. Thanks!!!

Rosanne Kosson  
 Patent Examiner, AU 1653  
 REM 3B84  
 571-272-2923  
 rosanne.kosson@uspto.gov

Aa 1076

PD: N119199 PCA

12/7/98 DE ? no

11/26/98 DE ? no

PCA/DE 90/03732

SOP32R  
URFESEARCHED  
INDEXED  
SERIALIZED  
FILED  
MAY 19 2006  
USPTO-CA5/22  
AT

ME

\*\*\*\*\*  
 Searcher: \_\_\_\_\_  
 Searcher Phone: \_\_\_\_\_  
 Date Searcher Picked up: \_\_\_\_\_  
 Date completed: \_\_\_\_\_  
 Searcher Prep Time: \_\_\_\_\_  
 Online Time: \_\_\_\_\_

\*\*\*\*\*  
 Type of Search  
 NA# \_\_\_\_\_ AA# \_\_\_\_\_  
 S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
 Encode/Transl: \_\_\_\_\_  
 Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
 Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
 Vendors and cost where applicable  
 STN: \_\_\_\_\_  
 DIALOG: \_\_\_\_\_  
 QUESTEL/ORBIT: \_\_\_\_\_  
 LEXIS/NEXIS: \_\_\_\_\_  
 SEQUENCE SYSTEM: \_\_\_\_\_  
 WWW/Internet: \_\_\_\_\_  
 Other (Specify): \_\_\_\_\_

Date completed: \_\_\_\_\_  
 Searcher: Beverly e 2528  
 Terminal time: \_\_\_\_\_  
 Elapsed time: \_\_\_\_\_  
 CPU time: \_\_\_\_\_  
 Total time: \_\_\_\_\_  
 Number of Searches: \_\_\_\_\_  
 Number of Databases: \_\_\_\_\_

## Search Site

\_\_\_\_ STIC  
 \_\_\_\_ CM-1  
 \_\_\_\_ Pre-S

## Vendors

\_\_\_\_ IG  
 \_\_\_\_ STN  
 \_\_\_\_ Dialog  
 \_\_\_\_ APS  
 \_\_\_\_ Geninfo  
 \_\_\_\_ SDC  
 \_\_\_\_ DARC/Questel  
 Other CGN

## Type of Search

\_\_\_\_ N.A. Sequence  
 \_\_\_\_ A.A. Sequence  
 \_\_\_\_ Structure  
 \_\_\_\_ Bibliographic

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GenCore version 5.1.8  
copyright (c) 1993 - 2006 Biocceleration Ltd.

## OM protein - protein search, using sw model

Run on: May 20, 2006, 17:05:42 ; Search time 320 Seconds  
(without alignments)  
3110.365 Million cell updates/sec

Title: US-09-856-723a-8

Perfect score: 5489

Sequence: 1 MKQYASPPMPTQTDVKLKFKP . . . . . RTLEQNKGKOMAKKEBKKVQLQ 1076

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext: 0.5

Searched:

2849598 seqs, 925115592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2;\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	5486	99.9	1196	2 Q6QNV2_HUMAN
2	5442.5	99.2	1231	2 Q8NDL1_HUMAN
3	5266	95.9	1160	2 Q6NXY2_HUMAN
4	4919	89.6	962	2 Q9Y9T7_HUMAN
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9	4265.5	41.3	1036	2 Q4SGB9_TEETING
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13	1127	20.5	771	2 Q9PM55_MOUSE
14	1082	19.7	723	2 Q8C2W6_MOUSE
15	1076.5	19.6	987	2 Q9V7X1_DRONC
16	1075.5	19.6	987	2 Q8MR93_DRONC
17	1018.5	18.6	987	2 Q7PKB6_ANOCA
18	965.6	17.6	310	2 Q9W119_HUMAN
19	~950.5	17.3	1716	2 Q9PM57_MOUSE
20	945.5	17.2	1415	2 Q9HTW7_HUMAN
21	941.5	17.2	1510	2 Q8N314_HUMAN
22	895	16.3	308	2 Q5QK22_MOUSE
23	850.5	15.5	1919	2 Q4RIP0_TEETING
24	627	11.4	125	2 Q53TG7_HUMAN
25	579.5	10.6	288	2 Q4SGC0_TEETING
26	556	10.1	243	2 QBTB83_HUMAN
27	507.5	9.2	1010	2 Q9VU34_DRONC
28	498.5	9.1	863	1 MILKL_HUMAN
29	480.5	8.8	967	2 Q6GNGU_XENIA
30	480	8.7	870	1 MILKL_MOUSE
31	467.5	8.5	1886	2 Q4T7H5_TEETING

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4	4919	89.6	962	2 Q9Y9T7_HUMAN
5	4683.5	85.3	1242	2 Q69W3J_MOUSE
6	4522	82		

Db	361 RYKRRKAPAPPVPLSPKGVLNNTVAGKQDLSSTPKPSPISPVLRGKPNAS QSLWCKE	RG The German cDNA Consortium;
ID	301 VTKOYRGVKITNFITSWRNGLSCAHLHRRPDLIDYKSINPOIKENNKAYGFASTG	RA Oettewelder B., Obermaier B., Deutschenbaur S., Schaiapp A.,
AC	421 VTKOYRGVKITNFITSWRNGLSCAHLHRRPDLIDYKSINPOIKENNKAYGFASTG	RA Meves H.W., Weil B., Amid C., Osanger A., Robo G., Han M., Wiemann S.,
DT	421 NSSYDQEKTYYAELDLKREPELLOPISGAVIDPLSODDSYFVNDSGVGESES	RL Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DE	421 NSSYDQEKTYYAELDLKREPELLOPISGAVIDPLSODDSYFVNDSGVGESES	[2]
Q9Y	541 NSSYDQEKTYYAELDLKREPELLOPISGAVIDPLSODDSYFVNDSGVGESES	RR NUCLEOTIDE SEQUENCE.
Db	481 ISRLIPSPDMVLLAIPDKLTWMTYQIRAHFSQBLNVQIEENNSKSTYKVNEYDT	RA Castellano-Munoz M., Fernandez-Chacon R.,
Q9Y	481 ISRLIPSPDMVLLAIPDKLTWMTYQIRAHFSQBLNVQIEENNSKSTYKVNEYDT	RL Submitted (TUN-2003) to the EMBL/GenBank/DDBJ databases.
Db	421 SPSTASPYCRTKSDTEPKQSQSGRTGSDDPGICSMPTDSTAQVULGKOLKAETL	CC Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>
Q9Y	601 SPSTASPYCRTKSDTEPKQSQSGRTGSDDPGICSMPTDSTAQVULGKOLKAETL	CC Distributed under the Creative Commons Attribution-NonDerivs License
Db	601 TSLIPTSKLGYSYSRDLIQLAKKKHASLRTESDSDADRTLNHADHSKIVQHLLSQB	CC DR
Q9Y	721 TSLIPTSKLGYSYSRDLIQLAKKKHASLRTESDSDADRTLNHADHSKIVQHLLSQB	DR EMBL; AL833968; CAD38814.; -; mRNA.
Db	661 ELSLYVSKKKDQNSPPFICEETBQKLUQDLSNEKEKLNSLECRSPESPIK	DR EMBL; AV331186; AAQ97141.1.; -; mRNA.
Q9Y	661 ELSLYVSKKKDQNSPPFICEETBQKLUQDLSNEKEKLNSLECRSPESPIK	DR EMBL; BAA00000115504; Homo sapiens.
Db	781 ELKERRARVILLEQARRDAALKAGNGKNTATPFCNRQDQBERRIQRLERARQIAR	DR HGNC; CH144; EMBL.
Q9Y	781 ELKERRARVILLEQARRDAALKAGNGKNTATPFCNRQDQBERRIQRLERARQIAR	DR InterPro; IPR001715; Calponin_act_bp.
Db	721 ARSGVOMSLPSGEMAEKKERSKASGDBNDIEIDNEIPEGFVGGDELNLN	DR Pfam; P00307; CH; 1.
Q9Y	841 ARSGVOMSLPSGEMAEKKERSKASGDBNDIEIDNEIPEGFVGGDELNLN	DR SMART; SM00033; CH; 1.
Db	781 DLDTPEQNSKLVDLKLKKLBVOPQVANSPSSAAQAVTESRSRDMKGKTEDLTERLQK	DR PROSITE; PS0021; CH; 1.
Q9Y	901 DLDTPEQNSKLVDLKLKKLBVOPQVANSPSSAAQAVTESRSRDMKGKTEDLTERLQK	DR Hypothetical protein.
Db	841 TTERPRNPYVPSKOSTVRKIQLOSFSQYIENRPEMKRSIORDTKKENKEKAI	DR DR
Q9Y	900 TERPRNPYVPSKOSTVRKIQLOSFSQYIENRPEMKRSIORDTKKENKEKAI	DR KRW Sequence 1231 AA; 139858 MW; DB7A7DBB672ABBB9 CRC64;
Db	961 TTERPRNPYVPSKOSTVRKIQLOSFSQYIENRPEMKRSIORDTKKENKEKAI	DR Query Match 99.2%; Score 5442.5; DB 2; Length 1231;
Q9Y	960 TTERPRNPYVPSKOSTVRKIQLOSFSQYIENRPEMKRSIORDTKKENKEKAI	DR Best Local Similarity 96.6%; Pred. No. 4.1e-205; Matches 1073; Conservative 1; Mismatches 2; Indels 35; Gap 1;
Db	121 MKQYASPMPTQDVKLKPLSKRKVSALQFSLCIFLRECKATBDMQSLASVSMKQ	DR DR
Q9Y	121 MKQYASPMPTQDVKLKPLSKRKVSALQFSLCIFLRECKATBDMQSLASVSMKQ	DR DR
Db	61 ADICNTLDPEDPENEDDENRBNQEBKAKIT-----	DR DR
Q9Y	181 ADICNTLDPEDPENEDDENRBNQEBKAKIT-----	DR DR
Db	92 -----ELINKUNPLDABEAKLATVNSNPPDPAELENPPCGDPDSEPERITETASPRKE	DR DR
Q9Y	92 -----ELINKUNPLDABEAKLATVNSNPPDPAELENPPCGDPDSEPERITETASPRKE	DR DR
Db	241 SASSEBELLINKUNFLVERAKDLATVNSNPPDPAELENPPCGDPDSEPERITETASPRKE	DR DR
Q9Y	241 SASSEBELLINKUNFLVERAKDLATVNSNPPDPAELENPPCGDPDSEPERITETASPRKE	DR DR
Db	146 DSYNNNSINPFGKEVQTYQLYNPFDEPERFTKDSQQSTKRNIRPVDMKLYADSK	DR DR
Q9Y	146 DSYNNNSINPFGKEVQTYQLYNPFDEPERFTKDSQQSTKRNIRPVDMKLYADSK	DR DR
Db	301 DSFNNNNPFPKEVQTYQLYNPFDEPERFTKDSQQSTKRNIRPVDMKLYADSK	DR DR
Q9Y	301 DSFNNNNPFPKEVQTYQLYNPFDEPERFTKDSQQSTKRNIRPVDMKLYADSK	DR DR
Db	206 TSEEBELDSBSNPFPKEVQTYQLYNPFDEPERFTKDSQQSTKRNIRPVDMKLYADSK	DR DR
Q9Y	206 TSEEBELDSBSNPFPKEVQTYQLYNPFDEPERFTKDSQQSTKRNIRPVDMKLYADSK	DR DR
Db	361 TEEBEDDSBNPFPKEVQTYQLYNPFDEPERFTKDSQQSTKRNIRPVDMKLYADSK	DR DR
Q9Y	361 TEEBEDDSBNPFPKEVQTYQLYNPFDEPERFTKDSQQSTKRNIRPVDMKLYADSK	DR DR
Db	266 AGKDLSTSPPKOSPIPSVPLGKPNASQSLLWCKEVTKMYGKUTNPITSWRNGLSPCA	DR DR
Q9Y	266 AGKDLSTSPPKOSPIPSVPLGKPNASQSLLWCKEVTKMYGKUTNPITSWRNGLSPCA	DR DR
Db	421 ASGDLSSTSPKESPIPSVPLGKPNASQSLLWCKEVTKMYGKUTNPITSWRNGLSPCA	DR DR
Q9Y	421 ASGDLSSTSPKESPIPSVPLGKPNASQSLLWCKEVTKMYGKUTNPITSWRNGLSPCA	DR DR
Db	326 ILHFRFDLIDYKSINPQDQIENNKAYGDFASIGTSRLLEPSDMVLLAIPDKLTWMTY	DR DR
Q9Y	326 ILHFRFDLIDYKSINPQDQIENNKAYGDFASIGTSRLLEPSDMVLLAIPDKLTWMTY	DR DR
Db	481 ILHFRFDLIDYKSINPQDQIENNKAYGDFASIGTSRLLEPSDMVLLAIPDKLTWMTY	DR DR
Q9Y	481 ILHFRFDLIDYKSINPQDQIENNKAYGDFASIGTSRLLEPSDMVLLAIPDKLTWMTY	DR DR
Db	386 YQIRAHFSQBLNVQIEENNSKSTYKVNEYDTDNSSVDOBKFYABSLDKREPELQ	DR DR
Q9Y	386 YQIRAHFSQBLNVQIEENNSKSTYKVNEYDTDNSSVDOBKFYABSLDKREPELQ	DR DR
Db	541 YQIRAHFSQBLNVQIEENNSKSTYKVNEYDTDNSSVDOBKFYABSLDKREPELQ	DR DR
Q9Y	541 YQIRAHFSQBLNVQIEENNSKSTYKVNEYDTDNSSVDOBKFYABSLDKREPELQ	DR DR
Db	446 ISGAUDPLSDQDSYFVNDSGVGESESBRQTDPLHSPSTASPYCRTKSDTEPKQS	DR DR
Q9Y	446 ISGAUDPLSDQDSYFVNDSGVGESESBRQTDPLHSPSTASPYCRTKSDTEPKQS	DR DR
Db	601 ISGAUDPLSDQDSYFVNDSGVGESESBRQTDPLHSPSTASPYCRTKSDTEPKQS	DR DR
Q9Y	601 ISGAUDPLSDQDSYFVNDSGVGESESBRQTDPLHSPSTASPYCRTKSDTEPKQS	DR DR
Db	506 GRTSSGDPGICSMNTSTQAVULGKRLKAETBLVSDKGKDMSPPICBETE	DR DR
Q9Y	506 GRTSSGDPGICSMNTSTQAVULGKRLKAETBLVSDKGKDMSPPICBETE	DR DR
Db	661 GRTSSGDPGICSMNTSTQAVULGKRLKAETBLVSDKGKDMSPPICBETE	DR DR
Q9Y	661 GRTSSGDPGICSMNTSTQAVULGKRLKAETBLVSDKGKDMSPPICBETE	DR DR
Db	566 QKQTDIGSNTLKEKLNSLECRSPESPIKTSPLSKLGYSYSRDLIQLKKA	DR DR
Q9Y	566 QKQTDIGSNTLKEKLNSLECRSPESPIKTSPLSKLGYSYSRDLIQLKKA	DR DR
Db	721 QKQTDIGSNTLKEKLNSLECRSPESPIKTSPLSKLGYSYSRDLIQLKKA	DR DR
Q9Y	721 QKQTDIGSNTLKEKLNSLECRSPESPIKTSPLSKLGYSYSRDLIQLKKA	DR DR
RP	NUCLEOTIDE SEQUENCE.	DR DR
RC	TRISSUS=Kidney;	DR DR
Q9Y	626 SLRQTESDDPADRTLNHADHSKIVQHLLSQBELLARVILLEQARRDAALKAGKHH	DR DR

Db	781	SLRQTESDPDPDRTTINHADHSISKVVOHRLISRQBELKERVILLEQARRDBALKAGNKH	RA	Director MGC Project;
RL			RL	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC			CC	
Qy	686	NTNTATPPCNCQQLSPQDERREROLERAROLAEARSQGUMSLSPLSGEMAAEKLERS	CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>
Db	841	NTNTATPPCNCQQLSPQDERREROLERAROLAEARSQGUMSLSPLSGEMAAEKLERS	CC	Distributed under the Creative Commons Attribution-NoDerivs License
Qy	746	KASGDENDNIEFIDTNEBIPGFVVGEGDELNLNLENDLTPEQNSKLVDJKLKGCLLEVQPO	DR	EMBL; BC067215; AAH67215.1; - ; mRNA.
Db	901	KASGDENDNIEFIDTNEBIPGFVVGEGDELNLNLENDLTPEQNSKLVDJKLKGCLLEVQPO	DR	HSSP; Q01082; IAA2.
Qy	805	VANSPSSAAQKVATTSSEODMSKGSGTEDIRTERLOCTTERFRNPVFSKUSTVKIQLQSP	DR	InterPro; IPR001715; Calponin_act_bd.
Db	961	VANSPSSAAQKVATTSSEODMSKGSGTEDIRTERLOCTTERFRNPVFSKUSTVKIQLQSP	DR	Pfam; PF00307; CH; 1.
Qy	866	SQYENRPEMKRSIQEDPKGKNGEKAETETQRKPSDEEVNGKPGKOTSQYUGELA	DR	SMART; SW0033; CH; 1.
Db	1021	SQYENRPEMKRSIQEDPKGKNGEKAETETQRKPSDEEVNGKPGKOTSQYUGELA	PROSITE; PS50021; CH; 1.	
Qy	926	LENEOKQIDTRALVERKLRYLMGTGRNTTEEEAMQEWMLVNKGNALTRMQLSL	SEQUENCE	SEQUENCE 1160 AA; 13232 MW; DD7923P0B14AF11 CRC64;
Db	1081	LENOKQIDTRALVERKLRYLMGTGRNTTEEEAMQEWMLVNKGNALTRMQLSL	Query	Query Match 95.9%; Score 566; DB 2; Length 1160;
Qy	986	KEDHDLERRYILNLTRALMAIEDPKTRAKKRQRFQFLDVLVALNKDALVEDDAOR	Best Local Similarity	Best Local Similarity 96.6%; Pred. No. 3.2e-198;
Db	1141	KEDHDLERRYILNLTRALMAIEDPKTRAKKRQRFQFLDVLVALNKDALVEDDAOR	Matches	Matches 1039; Conservative 1; Mismatches 0; Indels 36; Gaps 1;
Qy	1046	KQAREDEHEHLTLEONKGIAKKEKCVLQ	Db	1. MKQVQASPMPTQDTYKLKEPLSKKVSALQFSLSCIFREGKATDBMQSLASLWIKQ 60
Db	1201	KQAREDEHEHLTLEONKGIAKKEKCVLQ	Qy	1.21 MKQVQASPMPTQDTYKLKEPLSKKVSALQFSLSCIFREGKATDBMQSLASLWIKQ 180
RESULT	3	Q6NX72_HUMAN	AC	61 ADIGNLDDEBDNEDDENRNUOGEKAAKITELINKLNFLDEAKDQDATNSNPFDDPDA 120
Q6NX72_HUMAN		PRELIMINARY	DT	1.81 ADIGNLDDEBDNEDDENRNUOGEKAAKITELINKLNFLDEAKDQDATNSNPFDDPDA 240
Q6NX72_HUMAN		PRT	05-JUL-2004; Sequence version 1.	1.21 AELPFGDDSEEPITETASPRKTEDSFNSTNPKVEQVTPQINPDEPEARTVTKDS 180
Q6NX72_HUMAN		1160 AA.	DT	3.01 VTKQYRGVKLTINF'TSWNRGLSCAILHFRPDLVIDSYLNPODIKENKKAVDGFAIG 360
Q6NX72_HUMAN			DR	4.21 VTKQYRGVKLTINF'TSWNRGLSCAILHFRPDLVIDSYLNPODIKENKKAVDGFAIG 480
Q6NX72_HUMAN			GN	3.61 ISRLIEPSDMVLLAPDKLUTMITYLQYRAHFSQEBINVQIENSSTYKQNYEDT 420
Q6NX72_HUMAN			OS	4.81 ISRLIEPSDMVLLAPDKLUTMITYLQYRAHFSQEBINVQIENSSTYKQNYEDT 540
Q6NX72_HUMAN			OC	421 NSSYDQEKFYAEISDLKRPBPELOOPISGAVDFLSDODSVFUNDGVGVGESESEHQTPDHL 480
Q6NX72_HUMAN			OX	5.41 NSSYDQEKFYAEISDLKRPBPELOOPISGAVDFLSDODSVFUNDGVGVGESESEHQTPDHL 600
Q6NX72_HUMAN			NCBI_TAXID=9606;	4.81 SPSPASPCRTKSDTEPQKQSOSGRGSGDPPGICNTDQAQVILGKKLAKSTL 540
Q6NX72_HUMAN			RN	6.01 SPSPASPCRTKSDTEPQKQSOSGRGSGDPPGICNTDQAQVILGKKLAKSTL 660
Q6NX72_HUMAN			RP	5.41 BLSLYVSDKKMSPPFCEEDBQKQTLDGSNLKEKLNRSRCSRSPTRK 600
Q6NX72_HUMAN			RC	6.61 ELSLYVSDKKMSPPFCEEDBQKQTLDGSNLKEKLNRSRCSRSPTRK 720
Q6NX72_HUMAN			RT	6.01 TSLSPTSKLGYSYRSRDLIAKKHHSASLQTESDDADRTLNHADHSKIVORHLLSQE 660
Q6NX72_HUMAN			RT	7.21 TSLSPTSKLGYSYRSRDLIAKKHHSASLQTESDDADRTLNHADHSKIVORHLLSQE 780
Q6NX72_HUMAN			RT	6.61 ELKERRARVILLEQARRDAALKAGNKHNTATPPCNRQSDQDERREROLAE 720
Q6NX72_HUMAN			RL	8.41 ARSGVTKMLPLSPYGEMAAEKLERSKAG----- 869
Q6NX72_HUMAN			RL	7.81 ELKERRARVILLEQARRDAALKAGNKHNTATPPCNRQSDQDERREROLAE 840
Q6NX72_HUMAN			[2]	7.21 ARSGVTKMLPLSPYGEMAAEKLERSKAG----- 840
Q6NX72_HUMAN			RC	8.70 -----EQNSKLVDJKKGCLLVEQPVQVANSPPSSAQKVATTESSQDMKGSGTEDIRTERLOQ 924
Q6NX72_HUMAN			RP	NUCLEOTIDE SEQUENCE.
Q6NX72_HUMAN				"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences,"
Q6NX72_HUMAN				Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

Query Match 841 TTERFRNPVVFSDKSTVRKTQIQLQSFSQYIENRPEMKORSIQEDTKKGNEBEKAITEFOR 900  
 Best Local Similarity 89.6%; Score 4919; DB 2; Length 962;  
 Matches 962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 ID 0692W3\_MOUSE PRELIMINARY; PRT; 1242 AA.  
 AC 0692W3\_MOUSE  
 DT 13-SEP-2004, integrated into UniProtKB/TREMBL.  
 DR MKIAA0903 protein (fragment); Name=kbpl; Synonyms=mKIAA0903;  
 OS Mus musculus (Mouse).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthera; Buarchoontogires; Primates; Catarrhini; Hominoidea; Homo. NCBI\_TAXID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RD MEDLINE=99156230; PubMed=10048485; DOI=10.1093/dnareg/5.6.355;  
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hiroswa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; RT "Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.;" RL Ref. 5:355-364 (1998).  
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 DR EMBL: AB020710; BAA74926.1; -; mRNA.  
 DR RSP; Q01082; IBCR.  
 DR Ensembl; ENSG0000011504; Homo sapiens.  
 DR InterPro; IPR001715; Calponin\_act\_bdb.  
 DR SMART; SM00033; CH; 1.  
 DR PROSITE; PSS0021; CH; 1.  
 DR PON TER 1.  
 PT NONGEOMERIC  
 SQ SEQUENCE 962 AA; 109413 MW; 588B03150322D7AB CRC64;

RESULT 4  
 094977 HUMAN PRELIMINARY; PRT; 962 AA.  
 ID 094977  
 AC 094977  
 DT 01-MAY-1999, integrated into UniProtKB/TREMBL.  
 DT 07-FEB-2006, entry version 24.  
 DE KIAA0903 protein (Fragment).  
 GN Name=KIAA0903;  
 OS Homo sapiens (Human).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buthera; Buarchoontogires; Primates; Catarrhini; Hominoidea; Homo. NCBI\_TAXID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RD MEDLINE=99156230; PubMed=10048485; DOI=10.1093/dnareg/5.6.355;  
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hiroswa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; RT "Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.;" RL Ref. 5:355-364 (1998).  
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 DR EMBL: AB020710; BAA74926.1; -; mRNA.  
 DR RSP; Q01082; IBCR.  
 DR Ensembl; ENSG0000011504; Homo sapiens.  
 DR InterPro; IPR001715; Calponin\_act\_bdb.  
 DR SMART; SM00033; CH; 1.  
 DR PROSITE; PSS0021; CH; 1.  
 PT NONGEOMERIC  
 SQ SEQUENCE 962 AA; 109413 MW; 588B03150322D7AB CRC64;

RESULT 5  
 0692W3 MOUSE  
 ID 0692W3\_MOUSE PRELIMINARY; PRT; 1242 AA.  
 AC 0692W3\_MOUSE  
 DT 13-SEP-2004, integrated into UniProtKB/TREMBL.  
 DR MKIAA0903 protein (fragment); Name=kbpl; Synonyms=mKIAA0903;  
 OS Mus musculus (Mouse).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buthera; Buarchoontogires; Gires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.  
 DR NCBI\_TAXID=10090;  
 DR NUCLEOTIDE SEQUENCE.  
 RN [1]  
 RC TISSUE=Fetal brain;

Db 181 LWICIGEVTKNRYGVKINTFTSWRNLGFCATHHFRPLDLYKSLNPQDIRENNKAYD 240  
 Qy 355 GFSASIGSRLPSLSDMILALIDKUTMTYQIQRHFSGQBLNVOIEENNSKTYVG 414  
 Db 241 GFSASIGSRLPSLSDMILALIDKUTMTYQIQRHFSGQBLNVOIEENNSKTYVG 300  
 Qy 415 NYETDTNSVDSQDKFVAFSLKREPELQQPTSGAVDFFLSQODDSVFNDSGVGESSEHQ 474  
 Db 301 NYETDTNSVDSQDKFVAFSLKREPELQQPTSGAVDFFLSQODDSVFNDSGVGESSEHQ 360  
 Qy 475 TPDHHLPSSTASPYCRTKSDEPQKCSQSGRTSDDPGCNSNTSTQAVYLKRL 534  
 Db 361 TPDHHLPSSTASPYCRTKSDEPQKCSQSGRTSDDPGCNSNTSTQAVYLKRL 420  
 Qy 535 LKARTLEISDLVSKKKDMSPPICETDEBKQLQTLDIGSNLEKELENSRSLECRSDP 594  
 Db 421 LKARTLEISDLVSKKKDMSPPICETDEBKQLQTLDIGSNLEKELENSRSLECRSDP 480  
 Qy 595 ESPICKTSLSPLSKLGYSRQLDACKGHASLQTESPDADRTLNHADESSKIVQHR 654  
 Db 481 ESIKKITSLSPSKLGYSRQLDACKGHASLQTESPDADRTLNHADESSKIVQHR 540  
 Qy 655 LASRQEBSKERRAVLLEQARRDAALKAGKNGKINTTATPCNQRLQSLQDQDEERRRLERA 714  
 Db 541 LLSRQEBSKERRAVLLEQARRDAALKAGKNGKINTTATPCNQRLQSLQDQDEERRRLERA 600  
 Qy 715 ROLIARARSIVSNEELPSYGENAAEKURSKASGBENDNEFIDTNEEIPGFVWGGDE 774  
 Db 601 ROLIARARSIVSNEELPSYGENAAEKURSKASGBENDNEFIDTNEEIPGFVWGGDE 660  
 Qy 775 LTMLENDDUTPRONSKLWDKUKKLLVQPOVANSSSAAQAVTTESEQDMKSGTEDLR 834  
 Db 661 LTMLENDDUTPRONSKLWDKUKKLLVQPOVANSSSAAQAVTTESEQDMKSGTEDLR 720  
 Qy 835 TERLOKTTTERFRNPVVFSDKSTVRKTQIQLQSFSQYIENRPEMKORSIQEDTKKGNEBEKA 894  
 Db 721 TERLOKTTTERFRNPVVFSDKSTVRKTQIQLQSFSQYIENRPEMKORSIQEDTKKGNEBEKA 780  
 Qy 895 ITETQRKPSEDEVTLNGKFQTSQYVGEGLAALENBQKOIDTRALVEKRYLYMDGRT 954  
 Db 781 ITETQRKPSEDEVTLNGKFQTSQYVGEGLAALENBQKOIDTRALVEKRYLYMDGRT 840  
 Qy 955 EBBRMMQEWFLVNKGNAIRRMOQSLLEKEHDLERYRNLRMLAEDQKTE 1014  
 Db 841 EBBRMMQEWFLVNKGNAIRRMOQSLLEKEHDLERYRNLRMLAEDQKTE 900  
 Qy 1015 AOKRREGQDLDLVALVNLKRDALVRLDIAQEKAERBEDHELTERTLQNKKGKAKKEKCV 1074  
 Db 901 AOKRREGQDLDLVALVNLKRDALVRLDIAQEKAERBEDHELTERTLQNKKGKAKKEKCV 960  
 Qy 1075 LQ 1075  
 Db 961 LQ 962

RX Pubmed=15368895; DOI=10.1093/dnares/11.3.205;  
 RA Okarai N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoaka S.,  
 RA Saga Y., Seino S., Nishimura M., Kaihori T., Hoshino K., Kitamura H.,  
 RT Nagase T., Ohara O., Koga H.;  
 RT Prediction of the coding sequences of mouse homologues of KIAA gene:  
 RT IV. The complete nucleotide sequences of 500 mouse KIAA-homologous  
 RT cDNAs identified by screening of terminal sequences of 500 mouse KIAA-homologous  
 RT randomly sampled from size-fractionated libraries.;  
 RL DNA Res. 11:205-218(2004).

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DR EMBL; AKI73055; BAD32333.1; -; mRNA.  
 DR Ensembl; ENSMUSG00000042302; Mus musculus.

DR MGI; MGI-2667252; Ebhp1.  
 DR GO; GO:0005515; F\_protein\_binding; IPI.  
 DR InterPro; IPR01715; Calponin\_act\_bd.  
 DR Pfam; PF00307; CH; 1.  
 DR SMART; SM0033; CH; 1.  
 DR PROSITE; PS50021; CH; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 1242 AA; 140356 MW; 1C8D17FC63BC0932 CRC64;

Query Match 85.3%; Score 4633.5; DB 2; Length 1242;  
 Best Local Similarity 84.1%; Pred. No. 2.2e-175;  
 Matches 945; Conservative 40; Mismatches 78; Indels 61; Gaps 10;

QY 1 MKQVYASPMPTQTDVKLKFKPLSKKVVSAALQFSIICIFREGKAATDEDMOSLASLVMHQ 60  
 Db 132 MKQVYASPMPTQTDVKLKFKPLSKKVVSAALQFSIICIFREGKAATDEDMOSLASLVMHQ 191  
 QY 61 ADIGNLDDFEDNEDDENRNEQEEAKLT----- 91  
 Db 192 ADIGNLDDFEDNEDDENRNEQEEAKLTIVNQLNALSLSDBDDC1KQANVPSAK 251  
 QY 92 ----BLINKLNFLDAEKDLATINSNPPDDPAARIINPPGDDSERPTEETASPRKE 145  
 Db 252 SASSEBSELINTNLFEDEAKDLATINNPDEPDTPEVLAEPFGDDSEBPETTSPKKP 311  
 QY 146 DSFYNNSYNPKVEQTPQYIINPFDPEBEAFVTKIKOSPQSTKRKNTRPVMSKVYADSK 205  
 Db 312 BSFTNNSCPFPKGVQTPOIAPFDPETPFMVIKOSPPOSTRKRNLRPVMSKLYADSK 371  
 QY 206 TEERLDENSNPPYFPEKPT-SPPNLVNTVQEGETTERVRKRAPAPPAPLAPPAPPALT 253  
 Db 372 S-EBBELDESNPPYFPEKPT-SPPNLVNTVQEGETTERVRKRAPAPPAPLAPPAPPALT 429  
 QY 254 PKTGVLNENT-VSAGKDLSPKSPSIPSPVPLGRKPNASOSSLWCKEVTKNTRGVKTN 312  
 Db 430 PKGYV-NENTVWSAGKDLSPKSPKSPSIPSPVPLGRKPNASOSSLWCKEVTKNTRGVKTN 488  
 QY 313 FTTSWRNGLSSFCATAAHFRFDLIDYKSINPDKIENKNKAYDGASTIGSRLEPSDMV 372  
 Db 489 FTTSWRNGLSSFCATAAHFRFDLIDYKSINPDKIENKNKAYDGASTIGSRLEPSDMV 548  
 QY 373 LAIPDKLUTWYTLTQIRAMFSGQEANVOREENSSKSTYKVGETDTSVDOEKYAR 432  
 Db 549 LAIPDKLUTWYTLTQIRAMFSGQEANVOREENSSKSTYKVGETDTSVDOEKYAR 608  
 QY 433 LSDLKRPERLQQPSGAVDLSQDDSVFUNDGVSRSSESHQTDDHSPSTASPYCRT 492  
 Db 609 LSDLKRPERLQQPSGAVDLSQDDSVFUNDGVSRSSESHQTDDHSPSTASPYCRT 668  
 QY 493 KSDTRPQKSOQSGSGRTGSDPGICSNNTSTQAQVTLGKRLKARTLSDLVSDKCK 552  
 Db 669 KSDTRPQKSOQSGSGRTGSDPGICSNNTSTQAQVTLGKRLKARTLSDLVSDKCK 727  
 QY 553 DMSPPFICBETBDOKLQTLIGSLNEKEKLNSLCECSDPESPIKUPLSPSKLGS 612  
 Db 728 DVSP---LSAYEOKLOTHASASMEQKMKRSLSCLCRDGEALITKPNVSSPSKLG-- 781  
 613 YSRDLDLAKKKHASLQRQTESDPADRTTINHADHSKIVQHRLJSRQELKERARVLEQ 672

QY RESULT 6  
 OSSOK3 MOUSE  
 ID OSSOK3\_MOUSE PRELIMINARY; PRT; 1206 AA.  
 AC OSSOK3;  
 DT 21-DEC-2004; integrated into UniProtKB/TREMBL.  
 DT 21-DEC-2004; sequence version 1.  
 DT 07-FEB-2006; entry version 10.  
 DE Novel protein.  
 GN Name=RP23-51G7.3; ORFNames=RP23-51G7.3-001;  
 OS Mus musculus (Mouse);  
 OC Buxarota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Dunn M.;  
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Pelan S.;  
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
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DR EMBL; AL731880; CAA125563.1; -; Genomic\_DNA.  
 DR EMBL; AL669858; CAI25873.1; -; Genomic\_DNA.  
 DR EMBL; AL731880; CAA125573.1; JOINED; Genomic\_DNA.  
 DR InterPro; IPR001715; Calponin\_act\_bd.  
 DR Pfam; PF00307; CH; 1.  
 DR SMART; SM0033; CH; 1.  
 DR PROSITE; PS50021; CH; 1.  
 SQ SEQUENCE 1206 AA; 136234 MW; D49618A5DD5D2A82 CRC64;

Query Match 82.9%; Score 4552; DB 2; Length 1206;  
 Best Local Similarity 82.3%; Pred. No. 3e-170;  
 Matches 925; Conservative 39; Mismatches 74; Indels 86; Gaps 11;

QY 1 MKQVYASPMPTQTDVKLKFKPLSKKVVSAALQFSIICIFREGKAATDEDMOSLASLVMHQ 60

Db	121	MHQYASMPMQTDVKUKERPLSKVUNSATLQFSCIFIREKATIDDMOSLSLMSMKQ	180	
Qy	61	ADIGNLUDFEEEDDENVNQEEKAKit-----	91	
Db	181	ADIGNLUDFEEEDDENVNQEEKAKitTEUNQNALSLDEDODDCITRQANVPSAK	240	
Qy	92	-----ELINKNLFDEAEDKLTNSNPFDDPDAELNPFGDSEEPITETASPRKT	145	
Db	241	SASSBELINTNFIDEAEDKLTNSNPFDDPDAELNPFGDSEEPITETASPRKT	145	
Qy	146	DSFYNNSYNPKEVOTPOQLNPFPDEPFAVUTKDSPPOSTKRKNRIVDMSKLYADSSK	205	
Db	288	-----GVTQQLNPFPDEPFAVUTKDSPPOSTKRKNRIVDMSKLYADSSK	335	
Qy	206	TEREBELDESNPYPYERPEKPT-SPNLNVNTVOEGETERVRAAPAPPAPLAPPAPALT	333	
Db	336	S-EELIDESNPYPYERPEKPT-SPNLNVNTVOEGETERVRAAPAPPAPLAPPAPALT	393	
Qy	254	PKTGVLANTEN-VSAGKDLSTSPPSPVGKPNASQSLVWKEVTKYRGKTN	312	
Db	394	PKTGVLANTEN-VSAGKDLSTSPPSPVGKPNASQSLVWKEVTKYRGKTN	452	
Qy	313	FITSWRNGLSFCAILHFRPDLDIYKSLNPQDKKENKKATDGAFASIGSLPSDMVL	372	
Db	453	FITSWRNGLSFCAILHFRPDLDIYKSLNPQDKKENKKATDGAFASIGSLPSDMVL	512	
Qy	433	LSDLKREBPELQPIASAVDFISQDDSFVNUVGVBESERHTPDLSPSTASPICRT	492	
Db	573	LSDLKREBPELQPIASAVDFISQDDSFVNUVGVBESERHTPDLSPSTASPICRT	632	
Qy	493	KSDTPEOKQSOSGRSGSPDGICNTSDTORAVIDGKKULKAKTLESLDLYSKDKK	552	
Db	633	KSDTPEOKQSOSARTSGSDDPGLSSTDSDAQALASLGKKR-LKATNLIEJSDLCLVSDKK	691	
Qy	553	DMSPPFICBETEQQKOTLDTGSNLXEKLENSRSCECRSPESPCKTSLSPTSLGYS	612	
Db	692	DVSP--LSAEQKQTVHASSDMQGKMEKSRSCRLGELATTKPVNSPSPUG--	745	
Qy	613	YSDRLDIAKKKHSRQTESDDADPRTLNHADHSKIVORHLSSQBELCKERATLQE	672	
Db	746	YNRDTDTKKPCASLRQIESPDADKSTLNHADHPKAVORMLSSLQBELKERAVLLEQ	805	
Qy	673	ARRDAALKAGKHNTNTATPFCNRQLSQDQBERRQLERPARQLAEARSGVKMELPS	732	
Db	806	ARRDAALKAGKHNTNTATPFCNRQLSQDQBERRQLERPARQLAEARSGVKMELPS	865	
Qy	733	YGBMAEKLKERSKASGDENDNIEITDNEPEGFVGGBELTNLENDIJDTPBQNSKLV	792	
Db	866	YGBMAEKLKERSKASGDENDNIEITDNEPEGFVGGBELTNLENDIJDTPBQNSKLV	925	
Qy	793	DLKLUKLUVEPOVANSPSSAAQAKATBESSODMKSGTEDRTERQKTERFRPNUVS	852	
Db	926	DLKLUKLUVEPOVANSPSSAAQAKATBESSODMKSGTEDRTERQKTERFRPNUVS	985	
Qy	853	KDSTVKTKTQLOFSQYIENPEMKRQRIQEDTKKNEKEAITEORKPOSEDVLNKGP	912	
Db	986	KDSTVKTKTQLOFSQYIENPEMKRQRIQEDTKKNEKEAITEORKPOSEDVLNKGP	1042	
Qy	973	ALLRRNQNLSSLEKEEDLERYELLRELMLATIDWQKTAQKREQLLDEVALVN	1032	
Db	1103	ALLRRNQNLSSLEKEEDLERYELLRELMLATIDWQKTAQKREQLLDEVALVN	1162	
Qy	1033	KRDALYRDLAQKQEEEDHLERLTLQNKGKMKGEKVKLQ	1076	
Db	1163	KRDALYRDLAQKQEEEDHLERLTLQNKGKMKGEKVKLQ	1205	
Db	091ZU6	RESULT 7		
Mouse	091ZU6	MOUSE		
Preliminary	091ZU6	MOUSE		
PRT	091ZU6	MOUSE		
AC	091ZU6_7	MOUSE		
ID	091ZU6	MOUSE		
DT	01-DEC-2001		Integrated into UniProtKB/Trembl.	
DT	01-DEC-2001		sequence version 1.	
DT	07-FEB-2006		entry version 19.	
DE	KIAA093-3		KIAA093-3-like protein.	
GN	Name=Rhbp1; Synonyms=Ar424697;			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=C57BL/6J;			
RX	Medline:2235413; PubMed:12174196; DOI:10.1186/1471-2156-3-14;			
RX	Ruchs S., Resch K., Thiel C., Ulbrich M., Platzer M., Jockusch H.,			
RA	Schmitt-John T.,			
RT	"Comparative transcription map of the wobbler critical region on mouse chromosome 11 and the homologous region on human chromosome 2p13-14.";			
RT	BMC Genet. 3:4-14 (2002).			
CC	RHSP; Q01082; 1BKR.			
CC	MGI: MGI:2676252; Ehbpl.			
DR	GO: GO:0005515; P:protein binding; IPI.			
DR	InterPro; IPR001715; Calponin_act_bd.			
DR	PFam; PF00307; CH: 1.			
DR	SMART; SM0033; CH: 1.			
DR	PROSITE; PS50021; CH: 1.			
SQ	SEQUENCE: 1206 AA; CH: 1.			
Query Match	82.6%	Score 4532;	DB 2;	Length 1206;
Best Local Similarity	82.6%	Pred. No. 1.	88-169;	
Matches	922;	Conservative	39;	Nimatches 77;
				Indels 86;
				Gaps 11;
Qy	1	MHQYASMPMQTDVKUKERPLSKVUNSATLQFSCIFIREKATIDDMOSLSLMSMKQ	60	
Db	121	MHQYASMPMQTDVKUKERPLSKVUNSATLQFSCIFIREKATIDDMOSLSLMSMKQ	180	
Qy	61	ADIGNLUDFEEEDDENVNQEEKAKit-----	91	
Db	181	ADIGNLUDFEEEDDENVNQEEKAKitTEUNQNALSLDEDQDCIKQANVPSAK	240	
Qy	92	-----ELINKNLFDEAEDKLTNSNPFDDPDAELNPFGDSEEPITETASPRKT	145	
Db	241	SASSBELINTNFIDEAEDKLTNSNPFDDPDAELNPFGDSEEPITETASPRKT	287	
Qy	146	DSFYNNSYNPKEVOTPOQLNPFPDEPFAVUTKDSPPOSTKRKNRIVDMSKLYADSSK	205	
Db	288	-----GVTQQLNPFPDEPFAVUTKDSPPOSTKRKNRIVDMSKLYADSSK	335	
Qy	206	TEREBELDESNPYPYERPEKPT-SPNLNVNTVOEGETERVRAAPAPPAPALT	253	
Db	336	S-EELIDESNPYPYERPEKPT-SPNLNVNTVOEGETERVRAAPAPPAPALT	393	
Qy	254	PKTGVLANTEN-VSAGKDLSTSPPSPVGKPNASQSLVWKEVTKYRGKTN	312	
Db	394	PKTGVLANTEN-VSAGKDLSTSPPSPVGKPNASQSLVWKEVTKYRGKTN	452	
Db	313	FITSWRNGLSFCAILHFRPDLDIYKSLNPQDKKENKKATDGAFASIGSLPSDMVL	372	
Db	453	FITSWRNGLSFCAILHFRPDLDIYKSLNPQDKKENKKATDGAFASIGSLPSDMVL	512	
Qy	373	LAIPDLKLTWMTYQIRAHFSGQBLNVVOEEBSNSKSTKVGYETDTNSVQEEKAFAE	432	

RA Watson R.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 NUCLEOTIDE SEQUENCE.

RA Wilson R.R.;  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 CC  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonDerivs License  
 CC  
 DR EMBL; AC007098; AAV14789; 1; -; Genomic DNA.  
 DR Ensembl; ENSG00000115504; Homo sapiens.  
 DR InterPro; IPR011715; Calponin\_act\_bd.  
 DR PF00307; CH; 1.  
 DR SMART; SM0033; CH; 1.  
 DR PROSITE; PS50021; CH; 1.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 FT TBR 893  
 SQ SEQUENCE 893 AA; 100446 MW; 88B387A63176A52E CRC64;

Query Match 80.4%; Score 4414.5; DB 2; Length 893;  
 Best Local Similarity 97.5%; Pred. No. 5.4e-16;  
 Matches 864; Conservative 6; Mismatches 15; Indels 1; Gaps 1;  
 QY 66 LDDFREDND-DDENRVNOREKAATKITLETQKSEDEVLNKG 925  
 Db 8 LSSDEDQDCIKQANMRSAKSASSETELINKFLDEAKLATVNNSNPDDDFDAELN 67

QY 125 PFGDGPSPRITERATSPRKTEDSTONSNPKVQTYPINPDEPFRVTKIDSPPS 184  
 Db 68 PFGDPDSSEPTETASPRKEDSPNFSNPKNPKVQTYPINPDEPFRVTKIDSPPS 127

QY 185 TTKNIRPKDMSKLYADSKTEHELDENSNPFPKSTPPNNLVNPQBLERFRRVCR 244  
 Db 128 TTKNIRPKDMSKLYADSKTEHELDENSNPFPKSTPPNNLVNPQBLERFRRVCR 187

QY 245 KAPAPPVLSPTKPGVNLNTVSAGKDLSTSPKPSPIPSPVPLGRKENASQSLLVWCKEVTRN 304  
 Db 188 KAPAPPVLSPTKPGVNLNTVSAGKDLSTSPKPSPIPSPVPLGRKENASQSLLVWCKEVTRN 247

QY 305 YRGKLTINFTSWNGLSCIAILHFRPLIDYSINPDIKEUNKKAVGASIGSR 364  
 Db 248 YRGKLTINFTSWNGLSCIAILHFRPLIDYSINPDIKEUNKKAVGASIGSR 307

QY 365 LEPSDWMLAIPDKLTWMTYLQRAHSGQELNVQFENNSKTYKIGNYEDTNSV 424  
 Db 308 LEPSDWMLAIPDKLTWMTYLQRAHSGQELNVQFENNSKTYKIGNYEDTNSV 367

QY 425 DQEKEYAELSDLKRPELQOPTGAVDRFLSDQDSVVFUDGVVERSESEHOTPDDHLSPT 484  
 Db 368 DQEKEYAELSDLKRPELQOPTGAVDRFLSDQDSVVFUDGVVERSESEHOTPDDHLSPT 427

QY 485 ASPYCRRTKSIDTRPKSOSSGRSGSPGICNTDSTQAQVLGKRLLKETRLSD 544  
 Db 428 ASPYCRRTKSIDTRPKSOSSGRSGSPGICNTDSTQAQVLGKRLLKETRLSD 487

QY 545 LYVSDKKDMSPPTCIDEBOQLTDIGSNIKEKENSLECRSDPESITKKSLS 604  
 Db 488 LYVSDKKDMSPPTCIDEBOQLTDIGSNIKEKENSLECRSDPESITKKSLS 547

QY 605 PTSKLGYSYSSRDIDLAKKCHASLRQTESDPADRTLNAHDSSKIVORLISROEELKE 664  
 Db 548 PTSKLGYSYSSRDIDLAKKCHASLRQTESDPADRTLNAHDSSKIVORLISROEELKE 607

QY 665 RARVILEARRDAALKAKHNNTATPCNRQLSDQDDEERRQRRLQJAEASG 724  
 Db 608 RARVILEARRDAALKAKHNNTATPCNRQLSDQDDEERRQRRLQJAEASG 667

QY 725 VKNSELSPSGEMAAKLRKSKASGDEUNIEUDNEIPEGTVGGDELTLENDDT 784  
 Db 668 VKNSELSPSGEMAAKLRKSKASGDEUNIEUDNEIPEGTVGGDELTLENDDT 727

RESULT 8

Q3TV6\_HUMAN PRELIMINARY; PRT; 893 AA.

ID Q3TV6\_HUMAN PRELIMINARY; PRT; 893 AA.

AC Q3TV6\_

DT 24-MAY-2005, integrated into UniProtKB/TREMBL.

DT 24-MAY-2005, sequence version 1.

DT 07-FEB-2006, entry version 3.

DE Hypothetical protein KIAA0903 (Fragment).

GN Name=KIAA0903;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Gnathostomata; Amniota; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC Homo; Homo\_NCBITaxonID=9606;

RN [1]

RP NUCLEOTIDE\_SEQUENCE..

RA Kalicki J., Johnson D., Harris A.; Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RA Waterston R.H.; Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

RL NUCLEOTIDE\_SEQUENCE.

RP Waterston R.H.; Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

RL NUCLEOTIDE\_SEQUENCE.

QY 785 PEONSKLVDLKLUKLULEVOPQVANSPPSSAAQAVTESSEBQDMGSGTEDLTERLOKTER 844  
Db 728 PEONSKLVDLKLUKLULEVOPQVANSPPSSAAQAVTESSEBQDMGSGTEDLTERLOKTER 787  
QY 845 FRUUVVFESTVTRKTOLQSFSQYIENREPMKRSIQDTRKLKGNEENKAITETORKPSE 904  
Db 788 FRUUVVFESTVTRKTOLQSFSQYIENREPMKRSIQDTRKLKGNEENKAITETORKPSE 847  
QY 905 DEVLNKGKDTSQYVGEAALENEQKQDTRALVALVERKLRYIMDT 950  
Db 848 DEVLNKGKDTSQYVGEAALENEQKQDTRALVALVERKLRYIMDT 893

RESULT 9  
Q4SGB9\_ TETNG PRELIMINARY; PRT; 1036 AA.  
ID Q4SGB9\_ TETNG PRELIMINARY; PRT; 1036 AA.  
AC Q4SGB9\_ TETNG PRELIMINARY; PRT; 1036 AA.  
DT 19-JUL-2005, integrated into UniProtKB/TREMBL.  
DT 07-FEB-2006, entry version 4.  
DB Chromosome 17 SCAR14597 whole genome shotgun sequence.  
GN ORName=GSTENG001871001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontiformes;  
OC Tetradontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TAXID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed-15496914; DOI=10.1038/nature03025;  
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,  
RA Maucilon E., Bouneau L., Fischer C., Ozouf-Costa C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfallal G., Desat C., Segurens B.,  
RA Basiliau C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Bleumont C., Skalli Z., Cattolico L., Poulin J., De Berardinis V.,  
RA Craud C., Duprat S., Brottier P., Contarneau J.-P., Gouzy J.,  
RA Parra G., Lardier G., Chapple C., McKee K.J., McEwan P., Bosak S.,  
RA Kells M., Wolf J.N., Guigo R., Zody M.C., Meijer J., Robinson-Rechavi M.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D.,  
RA Laudet V., Schachter V., Quétier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.

RG Genoscope, Whitehead Institute for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
preliminary data.

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DR EMBL; CAAE0104597; CAG03033.1; -; Genomic\_DNA.

DR InterPro; IPR001715; Calponin\_act\_beta.

DR Pfam; PF00307; CH; 1;

DR SMART; SM0033; CH; 1;

DR PROSITE; PS50021; CH; 1;

DR SBQBCE; 1036 AA; 114819 MW; C1A8B829F17262B6 CRC64;

Query Match 41.3%; Score 2265.5; DB 2; Length 1036;  
Best Local Similarity 49.1%; Pred. No. 9.1.e-81; Mismatches 188; Indels 235; Gaps 30;  
Matches 524; Conservative 121; Misaligned 188; Indels 235; Gaps 30;

QY 1 MKOYASPMPTQTDVKLKEPKPLSKKVSAALQSLSCIFREGKATDEMDQSLASLVSMSKQ 60  
Db 32 MKOYASPMPTQTDVKLKEPKPLSKKVSAALQSLSCIFREGKATDEMDQSLASLVSMSKQ 91

RESULT 10  
Q5Q03\_ RAT PRELIMINARY; PRT; 762 AA.  
ID Q5Q03\_ RAT PRELIMINARY; PRT; 762 AA.  
AC Q5Q03\_ RAT PRELIMINARY; PRT; 762 AA.  
DT 04-JAN-2005, integrated into UniProtKB/TREMBL.

Db 92 ADIGNLDDPFEEENEDENKVNQBEAKATIVTFLTSFLVCFVALNLINKNPLFDQ 151  
QY 106 DL-A-TVNSNPFDPPDA---ELNP GDPDSRERPIETASPRKTESDFYNNSYAPFK--- 157  
Db 152 EASPMSTNFBPDSDLRHNRFPDPMDRERAPQPNSDLPNDHDSSNPEDP 211  
QY 158 --EVOTPOYLNPEDPELENVTIK--DSPPOSTKRKNTRPVDSKLYADSKYEEBDE 213  
Db 212 EPQLQTG--NPFDPEPDQTDLQDPDPBPKPRKRGVFPVDSKLYADVNEDELD 269  
QY 214 -----SNPYEPKSTPPRNVLVPOELFTERVYRKPA 249  
Db 270 FTQFLGCVNRSERNMNCHFCISLRSNPYEPKISSPAKPVQEG-PSLMSSQRRAPP 328  
QY 250 PVLSPKTG-----VIAENTVUSA-GKDL-STSP-----K 275  
Db 329 PSSPGKPPSPASKPVSSVPDREQALVGPSPTAVIGRELAASSPQMLQAVISLARK 388  
QY 276 PSPTPSPLVGRKENASQSLLVWCKEVTRVYRGVKTINFTSWSRNGLSFCALIHFREDLI 335  
Db 339 PSIIPSPPLGKGENASQSLVWCKEVTRVYRGVKTINFTSWSRNGLSFCALIHFREDVI 448  
QY 336 DYKSINPDKIENKKVADGFASIGTERLPSDMVIAIPDKLTWVMMYQIRAHSGQ 395  
Db 449 DYKSINPDKIENKKVADGFASIGTERLPSDMVIAIPDKLTWVMMYQIRAHSGE 508  
QY 396 ELVYQLENSSSKTYGVNEYDTNSVDPQEKFASLDRREPQQT---SGAVD 452  
Db 509 ELVYQLENSSSKTYGVNEYDTNSVDPQEKFASLDRREPQQT---SGAVD 568  
QY 453 LSQDDSV----FVNDGCVGESSEHOTPDHLSPTASPYCRTKSDETEPKSQSSGR 507  
Db 559 TKVEDGPKPDKCNVNDKAVTKLTKHQ---OSSPVTPS---RTVGTWSVDSOA--- 618  
QY 508 TGSDDPRICSNNTDSTQDQVILGKRLKAETBLSDIYVSDKRDMSPPFTCETBDQK 567  
Db 619 TPASEBERG-----SLTKANTLDSELSPQRERE----- 645  
QY 548 LQTDIGSNLEKYLENSR---SLECTSDPSPPIKTSLSPT---SKLGYSYSDILA 620  
Db 646 -----MEKEQQKOKVKGVEETNEGNTTSPSPGRGGPSPPHHQHOLGFSRNDAHLI 696  
QY 621 KKQHASLQTESDPADDE-TLNHAD-----SSKVQHLLSROBELKARR 667  
Db 697 KKCBASLHSSESPADSPCSPPPNHTPPQQPBTPTVTSLSAEKVLRSQBELKARR 756  
QY 658 VILLEQARDALAKAGNKINTNTATPCIN---RQLSDQODBERRQLRERARQLTAEARASGV 725  
Db 757 LLHEQARDAMAKSNKONPDSANAANISTTVCDERERRQLRERARQLTAEARASGV 816  
QY 726 KONSELPSTGEMAEALKL-ERSKASGDDNDIEIDTNEBIEPCFVUGGGDELNLENDDT 784  
Db 817 KONSELMSLIDPSGABRKGSKRTGPAADVIGVE-----GISE---ENID- 857  
QY 785 PEONSKLVDLKLUKLULEVOPQVANSPPSSAAQAVTESSEBQDMGSGTEDLTERLOKTER 844  
Db 838 -----SERGIGAGTADSHRE----- 873  
QY 845 FRUUVVFESTVTRKTOLQSFSQYIENREPMKRSIQDTRKLKGNEENKAITETOKPSE 903  
Db 874 VRNUVVFESTVTRKTOLQSFSQYIENREPMKRSIQDTRKLKGNEENKAITETOKPSE 933  
QY 904 PEONSKLVDLKLUKLULEVOPQVANSPPSSAAQAVTESSEBQDMGSGTEDLTERLOKTER 951  
Db 934 EEEVCPKPKDTSQYVGEAALENEQKQDTRALVALVERKLRYIMDT 981

DT 04-JAN-2005, sequence version 1.

DT 07-FEB-2006, entry version 12.

DB LOC309169 protein.

GN Name=LOC309169;

OS Rattus norvegicus (Rat).

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Rattus.

RN [1] -TaxID=10116;

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Heart;

RX MEDLINE:22388257; PubMed:12477932; DOI=10.1073/pnas.242603899;

RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,

RA Aleschul S.P., Zeeberg B., Buetow K.H., Schaeffer C.P., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Matsunaga K., Farmer T., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKenna K.J., Malek J.A., Gunnarino P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Hulyk S.W.,

RA Pailey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalacka U., Smialus D.B.,

RA Schinner A., Schein J.B., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.,";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Heart;

RG NIGC Project;

RL Submitted (DBG-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL: BC087115; AAH87115.1; -; mRNA.

DR Ensembl: ENSRNOG000000020788; Rattus norvegicus.

DR Interpro: IPR001715; Calponin\_act\_bd.

DR Pfam: PF00307; CH: 1.

DR SMART: SM00033; CH: 1.

DR PROSITE: PS50021; CH: 1.

SQ SEQUENCE 762 AA; 84105 MW; 1249FDT0B4BB886C CRC64;

Query Match 21.0%; Score 1154.5; DB 2; Length 762;

Best local Similarity 30.0%; Pred. No. 2.1e-37;

Matches 325; Conservative 104; Mismatches 205; Indels 449; Gaps 20;

QY 1 MKQVYASPMPTQTYKVKKPLSKKVMSALQPSLSCIPREKGAKTDQDQSLASIVSMQ 60

QY : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : 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: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : 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QY 301 VTKNYRGVKITNFETTSWRNGLSFCAILHIFPDLIDYKSLNPDKENRKAYDFGASIG 360

Db 267 VTGKIRGVCTINFTSWRNGLAFCAILHIFPDLIDYKSLNPDKENRKAYDFGASIG 326

QY 327 VSRLILPDAWVLISVPDKLIVMVTLCQIRAFCTQGQLQVOLQVEGGGGSTYRNAQQPSL 386

Db 420 --TNSVQDQEKFPAELSKREP-BLOOPISAVDPLSODDSVFNDSVGUGESERHQ 475

QY 387 PDCLANAGDIAQRLEHGARASTERKEAVNRGTGAIPKVASRDTDLGSSKDGRAEVAQA 446

Db 485 -----RLRS-SVNGEAGPV 498

QY 476 PDDHILSPSTATSPYCRTKEDTEPOKSQOSGSRTSGSDPGICSNSTDQVQVLLGKKRL 535

Db 447 ----VQBEASSDGPRARSSTSP--WVPTEGLINGVGAPASVSV----- 484

Db 596 SPIKKTSPLSPSKLGYSYRSRDLJAKKHASIROTESPDADRTLNADHSSKVQHRL 655

Db 499 PP-----PRAKOSFHSDRADLIKRSRLRNS----- 528

Db 656 LSROBELKERARVILLEQARRDAALKAGNKNTNTATPCFNCNQLSDQDERRROLRERAR 715

Db 529 ----- 528

QY 716 QLIAEARSGVTKMSLPSYGEMAAEKLRSKASGENDNEIDNEELPEGFVYGGDEL 775

Db 529 -----FSDVDDQS-----GTAVGAGPAG 546

QY 776 TNLENDLDPQEONSKLVDIUKLKKLULBVQPVQVANSPSSAQAVTSSBQDMKSGTEDLRT 835

Db 547 SGA---VGEPNPOSSLSDGTLTATAPOOPPSGPP----- 578

QY 836 ERLQKTTFRPNPVFSKQDSTVRKTQLOSFQXYTENRDEMKRQSIQDITKKGNNEKAII 895

Db 579 -----TEBSPNP----- 586

QY 895 TEORKPSIDEVNLKGFFDTQSYVQCAELQALEOBQGQIDRANEVEKQURSLMESGARNL 955

Db 587 -----GEEAGQRFQDTSQVCAELQALEOBQGQIDRANEVEKQURSLMESGARNL 638

QY 956 ERAMQHMFMLVKKNLRMQLSLKEDLERYLERYELERLMLAIDWQTERA 1015

Db 639 QEBLIOEQFTLVNLKNAIRRQDOLQLEBODLERPESRLRMLAERWKVTA 698

QY 1016 QKRBQOLLDEVALVNKEADYLDQKQBKEEDHLERTLEQNKGKMAK--KBRK 1072

Db 699 QKRBQOLLDEVALVNKEADYLDQKQBKEEDHLERTLEQNKGKMAK--KBRK 758

QY 1073 CVL 1075

Db 759 CTL 761

RESULT 11

Q93U97\_MOUSE PRELIMINARY; PRT; 874 AA.

ID Q93U97;

AC Q93U97;

DT 01-JUN-2001, integrated into UniProtKB/TREMBL.

DT 01-JUN-2001, sequence version 1.

DT 07-FEB-2006, entry version 19.

DB Tangerin B (LOC114601 version).

GN Name=Kcnk7;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Mus.

NCBI TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BABY/C;  
 RA Melichar J.M., Noegel A.A., Korenbaum E.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N TISSUE= Mammary tumor. C3;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold B., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Brat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heisler F.,  
 RA Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soates M.B., Bonaldo M.R., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley J., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muñoz D.M., Sodergren B.J., Lu X., Gibb R.A.,  
 RA Fahey J., Heilman B., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M.,  
 RA Butterfield S.Y.N., Krzywinski M.J., Skalska U., Smallius D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Mazzra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
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CC EMBL; AP305088; AAK32110.1; -; mRNA.  
 DR EMBL; BC004660; AAH04660.1; -; mRNA.  
 DR HASP; Q01082; 1BKR.  
 DR MGL; MG1:131841; Kcnk7.  
 DR GO; GO:0016021; C: integral to membrane; RCA.  
 DR GO; GO:0016020; C:membrane; RCA.  
 DR GO; GO:0005267; P:potassium channel activity; RCA.  
 DR GO; GO:0006813; P:potassium ion transport; RCA.  
 DR InterPro; IPR001715; Calponin\_act\_bd.  
 DR Pfam; PF00307; CH\_1.  
 DR SMART; SM00033; CH\_1.  
 DR PROSITE; PS0021; CH\_1.  
 DR SEQUENCE; 874 AA, 95561 MW, 94803958BCDF5B6D CRC64;

Query Match 21.0%; Score 1151.5; DB 2; Length 874;  
 Best Local Similarity 30.3%; Pred. No. 3.e-37;  
 Matches 337; Conservative 116; Mismatches 264; Indels 395; Gaps 27;

1 MKQVAPSPMPTQTDVKLKPKPLKKVVSALQFSLSCIPRLREGKATDMSQLASLVNQK 60  
 ; :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 120 LATHAGPQPAQVPLRURLKPKSKVWHALSITISGVILLEGRADDDMQSLSMSVKP 179

61 ADIGGNLDPEEEDDEDDENRVEBEKA-AKTTILINKUNFLRAKODLATVNSNPFDPP 119  
 ; :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 180 SDVGNLDDFAESDEBEEANGPAPBVRTRGPOSLSRELXTC-BEDBGHIR-----PO 232

120 ABALNPFGDPD-SEEPITETASPKTEDSPINNSYNPKEVQTPQVANPFDSPRAFTIK 178  
 ; :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 233 QAAARPSSAEDTSPAPVAPAPPVRA-----FRQQGSPIAATGQ 273

179 DISPOSTRKKNTRPVDMSKYLYADSSKTEBEBELDESNPYPKEPUSTPPRNLNLPVOLET 238  
 ; :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 274 VGP-----ETPEPPPSPP--ETNSTGQPGQTMWPT--AP 304

,QV 239 ERRVTKRKPAPPV-----LSPKINGVLMENTVSA-----GKDLS-SPSPKSPPIP 280

Db 305 RLRIKSDAPASSPPVPCSGDPPVNTSEDPPVPGMSSGETAQISSOEGTAHEARPEPDEA 364  
 QY 281 SPVLRGKPKNAQSOLIVWPKGEVKVNRGKVNNTTSNMGSLPCALIHRPDLIDYSL 340  
 Db 365 PTPL--VSQSSELEWQEQEVYRGCVTNTTSRNGLPCALIHRFVYPKDIDSL 421  
 QY STRAIN=FVB/N TISSUE=Mammary tumor. C3;  
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold B., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Brat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heisler F.,  
 RA Richards S., Morley J., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muñoz D.M., Sodergren B.J., Lu X., Gibb R.A.,  
 RA Fahey J., Heilman B., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M.,  
 RA Butterfield S.Y.N., Krzywinski M.J., Skalska U., Smaliius D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Mazzra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BABY/C;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
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CC EMBL; AP305088; AAK32110.1; -; mRNA.  
 DR EMBL; BC004660; AAH04660.1; -; mRNA.  
 DR HASP; Q01082; 1BKR.  
 DR MGL; MG1:131841; Kcnk7.  
 DR GO; GO:0016021; C: integral to membrane; RCA.  
 DR GO; GO:0016020; C:membrane; RCA.  
 DR GO; GO:0005267; P:potassium channel activity; RCA.  
 DR GO; GO:0006813; P:potassium ion transport; RCA.  
 DR InterPro; IPR001715; Calponin\_act\_bd.  
 DR Pfam; PF00307; CH\_1.  
 DR SMART; SM00033; CH\_1.  
 DR PROSITE; PS0021; CH\_1.  
 DR SEQUENCE; 874 AA, 95561 MW, 94803958BCDF5B6D CRC64;

Query Match 687 TNTATPFCNRQLSDQODPERRQLRERARQLTAEARSGVKNSLPSYGMMAEKLKERRSK 746  
 DB 638 SNSYS-----VDDQD-----SGAVANGPA-GPGAVE----- 663

QY 747 ASIDBDNDIEIDTNEBEPBEGFVGGSDPDELNLENDLDTPEONSKLNUKLKULLEYQFOV 806  
 DB 664 -----GPNP 667

QY 807 ANSPSSAAKAVTESSBQDMKGSTEDIRTERIQLKTERFRNPVVPFSKDSVTKTQLOFS 866  
 DB 693 --ESSISLGEGEAGLQR-----PQTSQVCAEQLQ 721

QY 668 ASDDANEPLAPVVPQBPQGPGRPPE----- 692

QY 867 QYENRPEMKRPSIQEDTKKGNEEKAAITEQTKSEDEVLNKGFKDTSQVVGELAL 926  
 DB 722 EQGQGQIDGRANEVEKQLRSMEGANRQLOSERVLIQFWFLVNKQNALIRRNLQSLIEK 986  
 QY 987 EHDLERVYELLERELRMLATEDWQKNEAEKEREQOLDELVALVNRDVALVDRDQEK 1046  
 DB 782 EODLERVELLUSRELMALATEEWQKTYVAQDREQLQBLVLSVQNRDDELVRDQEK 841  
 QY 1047 QAEEDDEHLERTLEQNKCKMAK---KEEKCVL 1075  
 DB 842 LALEEDERLRLERLQEQRKVKSQLSRERCIL 873

RESULT 12

Q99MS6\_MOUSE  
 ID Q99MS6\_MOUSE PRELIMINARY; PRT; 759 AA.  
 AC Q99MS6  
 DT 01-JUN-2001, integrated into UniProtKB/IT-EMBL.  
 DT 01-JUN-2001, sequence version 1.  
 DT 07-FEB-2005, entry version 17.

DB Tangerin C.  
 GN Name=Kcnk7;  
 OS Mus musculus (Mouse);  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Muroidea; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10990;  
 RN [1] NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BALB/C;  
 RA Melchior J.M., Noegel A.A., Korenbaum E.;  
 RL Submitted (SSP-2000) to the EMBL/GenBank/DBJ databases.  
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 DR EMBL; AF0205089; AAK32111.1; -; mRNA.  
 DR HSSP; Q01082; 1BKR.  
 DR Ensembl; ENSMUSG0000024937; Mus musculus.  
 DR MGI; MGI:1341841; Kcn7.  
 DR GO; GO:0016021; C:integral to membrane; RCA.  
 DR GO; GO:0016020; C:membrane; RCA.  
 DR GO; GO:0005267; P:potassium channel activity; RCA.  
 DR GO; GO:0006813; P:potassium ion transport; RCA.  
 DR InterPro; IPR001715; Calponin\_act\_bd.  
 DR Pfam; PF00307; CH; 1.  
 DR SMART; SM00033; CH; 1.  
 DR PROSITE; PS50021; CH; 1.  
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 Best Local Similarity 29.8%; Pred. No. 1.8e-36;  
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 QY 1 MKQVQASPMPTQTDVKLKFKPKPSKVVVASALQPSLSCIPLREGKATDEDMOSLASIVSMQ 60  
 120 LAHHAGPVPQVPLRKLKPKPSKVVVASALQPSLSCIPLREGKATDEDMOSLASIVSMQ 60  
 Db 61 ADIGMUDPFDPEBDDENWQNQEKAKITBLINKNLFDBARKDLATWNNTNPDDPA 120  
 Db 180 SDVGNDLDRFASDES----- 194  
 121 AELNPFGDPDSBEPITETASFRKTEDSFVNNSYNPKEVOTQVLNPFDPEAFVTKQS 180  
 195 -EANGRGPAE----- 207  
 Db 181 PPOSTKRNIPRVDMSKYLAADSCTKEERBLIDESNPFPYRKPSTPPRNPNLYNPVOLER 240  
 208 GPQS-----DLISREL-----KTCBEEDEGH-----IRPQQ----- 233  
 Db 241 RVRKKAPAPPVLSPTKPGVNLNTSAGKOLSTSPPKSPPPSVLGRKPNASQSLIVCKE 300  
 234 -----AAAPC-----SSAEP-----TSPAP-----PTL-----VASSQSLWCR 266  
 301 VTKNVRGVKINTFTSWRNGLSCAHLHRRPDLDYKSLNPODKKENKKAYNGPASTG 360  
 267 VTINGRPGVCINFTFTSWRNGLCAFCAHLHRYFPDKDIFSLDPLNIKQNNQAFQGA LG 326  
 QY 361 ISRLRPSDMLLAPDKLUTMVTYQTRHPSGQBLYNVIQIERNNSKSTYKVGYETDT 420  
 327 VSRLLEPADMLLVSVDKLUVMTICQIRAPTQGOBLQVOLQEGGGSGTYRVNAQSL 386  
 Db 421 NSSVQDKFVAFSLDKREPELQPI-----SGAVDPLSODDSVRFNSCVGBERS 471  
 QY 387 PDCDA----GDLAQRLRBRGEAVTERKEAVNGTGAIKPVAQRDTPDISCSKDGRAB- 441  
 DR InterPro; IPR001715; Calponin\_act\_bd.  
 DR Pfam; PF00307; CH; 1.  
 DR SMART; SM00033; CH; 1.  
 DR PROSITE; PS50021; CH; 1.  
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 Best Local Similarity 29.8%; Pred. No. 2.6e-36;

Matches	327;	Conservative	108;	Mismatches	195;	Indels	46;	Gaps	26;
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Db	120	LASHHAGPVAQVPLRLKEPSKVVKVHABLSLTSGVLLREGRAANDDMQSASLMSVKP	179						
Oy	61	ADIGNLDPFEDNDDERVNQSEKAATIELINKNLFLDAEKDLATVNNSNPDDFA	120						
Db	180	SDVENTDDPFSRDE-----	194						
Oy	121	AELNPFGDDSEEPITETASPRKTEDSFNNNSYNPKEVQTPQVLPNPFDEPEAFVTIKDS	180						
Db	195	-EANGGATE-----	207						
Oy	181	POSTK---RKNIRPVDMWSKYLADSSKTEEEELDESNNPYPKSTPPNNLNPNVQBL	236						
Db	208	GPOSGRGCAPLRLGPP-DLSREL-----KYLCEBEGH-----TRPOO--	245						
Oy	237	BTERRVKRKGAPAPVPLSPKTVGMENTVSAGKOLSTSPPSPSIPSPVGLRKPNASILV	296						
Db	246	-.....AAARP-----SSA-----TSPAP----PTL----VASSQSL	274						
Oy	297	WCKEVTKNYRGKVTNFSTSWRNGLSPCATLHFRPDLDYKSLANPQDTKENNKAYGP	356						
Db	275	WCQEVINGYRGCVCTNFTSWRNGLFCATHHFRPDLDYKSLANPQDTKENNKAYGP	334						
Oy	357	ASTGISRLRAPSMDVTLAIPDPLKUTWVYQIRAHPSQOELNVYQIERNSSKTYKVN	416						
Db	335	ALGVSRILLEPDAWVLSPVDPKLWTMTCQIRACTGQELQLVQLEGGGSGTYRVNA	394						
Oy	417	ETDUNNSVTDQKRYAELSLKREPELQOI-----SGAVDPLSDQDSVFNDSVG	467						
Db	395	QPSLPLCJLA-----GDAQRLRHRGAEVTPKRAVNRGTGAIPKVASRDTLSCSSKG	450						
Oy	468	BSESBHQTPDDHLSPSTASPYCRTKSQDTEPKQSOQSSGRTSQSSDPP-----GICSNNTS	522						
Db	451	EAE-----VAQEAIQEAQPTGDRARASSTTPVPAEGIVNGYA	489						
Oy	523	TQAQVLGLKRLKRLKAEETLBSLVDYVSDKKKDMSPPPICETBDQKLQTLDIGSNLEKRL	582						
Db	490	S-----GSVLRRS-----	498						
Oy	583	ENSNSLECSRDSPESPIKTSLSPIKSYSSRDLAKRKHSILQTESPDPADRTIN	642						
Db	499	---SVNGRAGPVPP-----PRAGHSFHVBDLACKRSRLR-----	533						
Oy	643	HADHSKIVQHRLSROBELLKERAVLLEQARRDAALKAKGKNTNTATPPCNQRLSDQ	702						
Db	534	-----NSNS-----NSNS-----VVDQ	543						
Oy	703	DEERRRQLRERARQLIAEARSQVMSELSYGEAAKUKERSKASGDNDNIEIDTNEB	62						
Db	544	D-----SGAAGGAGPA-GPAG-----	560						
Oy	763	IPECFFVGGDELNLENDLDPFQNSKUVDLKKGKJLVEQPVANSQSSAAMQAVTESS	822						
Db	561	-----GPNFZASSPDANPLPAPVPOQ	580						
Oy	823	BQDMKSGTBEDLRLRQLKTFRFPVVFSKDSVTKTOLQSQYQVIRPEMKRSIQ	882						
Db	581	PPEGPPPT-----ESSPLGREGLO	602						
Oy	883	EDTKKGKGNBKAIAITETORKPSSEDEVLNKGPKFDTSQYVUGELALEENEQDQITFRAALVEK	942						
Db	603	R-----FQDLSQYVCABLAQALEOEGQQIGRAAEVEK	634						
Oy	943	RLLYLYMDGGRNTTREBAMQEWEMUNVKONALRRMNGLSLKEKDHLLERVELNRLR	1002						
Db	635	QLRSIMESGANLQEEVLIQEWTFUNVKONALIRRQDOLQLLTEQDLRFLSLR	694						
Oy	1003	AMLAIEDWQTKTEAQKREOLLDELVALVNLKDVALVRLDQDAQKQABEDEHIELTQN	1062						
Db	695	AMLAIEEWQKTAQHREQOLLEBLVSLVNQDDELVRLDQKERIALBEDERLURGLER	754						

RN

[3]

- RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary;  
 RX PubMed=16141073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group  
 "Genome Network Core Team) and the FANTOM Consortium;  
 RT "Antisense Transcription in the Mammalian Transcriptome.";  
 RL Science 309:1564-1566(2005).  
 RN [4]
- RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary;  
 RX MEDLINE=23354683; PubMed=12456851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 Nikido I., Osato N., Saito R., Suzuki H., Yamamoto I., Kyobashi H.,  
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,  
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 Sandelin A., Schneider C., Semple C., Seto M., Shimada K.,  
 Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 Verardo R., Wagner D., Wahlestedt C., Wang Y., Wattanavee Y., Wells C.,  
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 Shiraki T., Wakai K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 Hara A., Hashizumi W., Imotani K., Ishii Y., Itoh M., Kagava I.,  
 Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,  
 Yasunishi K., Hayashizaki Y., Hayashizaki Y., Hayashizaki Y.,  
 Birney E., Hayashizaki Y., Hayashizaki Y., Hayashizaki Y.,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 NTRE 420:563-573 (2002).  
 RN [5]
- RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary;  
 RX MEDLINE=21084660; PubMed=11211851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 Akatawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 Aizawa K., Iizawa M., Nishi K., Kyozuka H., Kondo S., Yamamoto I.,  
 Saito T., Okazaki Y., Bono H., Kasukawa T., Saito R.,  
 Kadota K., Matsuda H.A., Ashburner M., Batyalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 Kuehl P., Lewis S., Maturov Y., Nitaya T., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Stuhli P., Suzuki R., Tomita M., Wagner J., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barth G.,  
 RA Blaize J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guselnichka S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Maslima M., Mazzarella J.J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez J., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seye T., Shihata Y., Storch K.-F.,  
 RA Wynnshaw-Boris A., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Hayashizaki Y., Hayashizaki Y., Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 RN [6]
- RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary;  
 RX MEDLINE=20499574; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayashizaki Y., Sugahara Y., Shibata K., Itoh M.,  
 RA Kano H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).
- RN [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary;  
 RX MEDLINE=2053013; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibusawa K., Itoh M., Alzawa K., Nagaoaka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitaunai T., Tachiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsubara S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inouye Y., Kira A., Hayashizaki Y.,  
 RT "RIKEN integrated sequence analysis (RISA) system-3Ba-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RR Genome Res. 10:1757-1771 (2000).  
 RN [8]
- RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary;  
 RA Adachi J., Alzawa K., Akimura T., Aratawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hara A.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirayama T., Hirokawa T.,  
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kurokawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Obata N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagami A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi K., Muramatsu M., Hayashizaki Y.;  
 RR Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
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 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC EMBL; AK087817; BAC40012.1; - ; mRNA.  
 DR HSSP; Q01082; IBKR.  
 DR MG1; MGI:1341841; Kcn7.  
 DR InterPro; IPR001715; Calponin\_act\_bp.  
 DR Pfam; PF00307; CH; 1.  
 DR SMART; SM00033; CH; 1.  
 DR PROSITE; PS50021; CH; 1.  
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 Db 96 KLNFLDEBARDLDTVNNSPFDDDAEAEUNPFGPDP-SERPIETEPASPRITEPDSFYNNYN 154  
 QY 62 ELKTLCE-BEDEGHIR----POQAARAPSSAEDTSAPVSAAPPVRA----- 104  
 Db 155 PPKEVQTPQYINPDEPERAVFTKOSPOSTKRKNIRVUDMSKVLYASSKTSERELBS 214  
 105 -----FRGDGSPEPARAITGSGVGVP----- 130  
 DB 215 NPFTVBPKSTPPPNLVLNPVOBLETERVVKRKAAPPV-----LSPKTVGVLNT 263  
 QY 131 PP--ETRSIQCPGQTMVPP-APRLRKGSDAASSPPVCSGDEVPNTSSEDPPTGMSGGE 186  
 264 VSA-----GKDL-STSPKSPRSPVSPVGRKPWASQSLIVWCKEVTKYRGVKTNTS 316  
 DB 187 TQAOISSLSSORGTEAHEARTPBDIEAPPL---VSSSQSLIEWCQBVNTSYRGVCITNFNTS 243  
 QY 317 WRNGLSPCAILHHRPDLDYKSLNPQDIKENKKAYGPGASTIGISRLIEPSDMVLLAIP 376

- RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,  
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 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotrier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Decher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dobson K., Douc L.B., Downes M., Dusen-Rocha S., Dunkov B.C., Dunn P.,  
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 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
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 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitt A., Li J.-H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moskatev A.,  
 RA Mount S.M., Moy M., Murphy L., Muzyk D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
 RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Schiebler F., Shen H.,  
 RA Shue B.C., Siden-Kiamas I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirska R., Tector C., Turner R., Venter C., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhao G., Zhao L.,  
 RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426055; PubMed=12537568;  
 RA Celinker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champé M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Laverty T., Muzyk D.M., Nelson C.R.,  
 RA Pacleb J.M., Park S., Preiffier B.D., Richards S., Sodergren E.J.,  
 RA Svirska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstock G., Scherer S.B., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
 melanogaster euchromatic genome sequence.,"  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirska R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celinker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 a genomic perspective.,"  
 RL Genome Biol. 3:RESEARCH0084-1-RESEARCH0084.20(2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky T., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whittfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bettencourt B.R., Celinker S.E., de Grey A.D.N.M., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 systematic review.,"  
 RL Genome Biol. 3:RESEARCH0083-1-RESEARCH0083.22(2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20196006; PubMed=10731137; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ammanatides P.G., Scheer S.R., Li P.W., Hoskins R.A., Galle R.P.,  
 RA George R.A., Lewis S., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA NCBI TAXID=227;
- RESULT 15  
 Q9V7X1\_DROME PRELIMINARY; PRT; 987 AA.
- ID Q9V7X1; AC 0; DT 01-MAY-2000, integrated into UniProtKB/TREMBL.  
 DT 05-JUL-2004, sequence version 2.  
 DT 07-MAR-2006, entry version 26.  
 DB CG15609\_PA, isoform A (Cg15609\_pb, isoform b).  
 GN ORFNAME=CG15609, Dmel CG15609;  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Diptera; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydioidea; Drosophilidae; Drosophila.  
 OC NCBI TAXID=227;
- RN [1]
- RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20196006; PubMed=10731137; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ammanatides P.G., Scheer S.R., Li P.W., Hoskins R.A., Galle R.P.,  
 RA George R.A., Lewis S., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA NCBI TAXID=227;
- RN [2]
- RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20196006; PubMed=10731137; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ammanatides P.G., Scheer S.R., Li P.W., Hoskins R.A., Galle R.P.,  
 RA George R.A., Lewis S., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA NCBI TAXID=227;



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Abg22881 Novel hum  
Abg55396 Human MDD  
Abdc31335 Human nov  
Ham1727 Peptide #  
Abb36228 Peptide #  
Abb31040 Peptide #  
Ham69395 Human bon  
Ham57004 Human bra  
Abg51067 Human liv  
Ham04922 Peptide #  
Abg39012 Human pep  
Ab60197 Human gen  
Ab65591 Drosophil  
Abd48312 Drosophil  
Abp9856 Human str  
Abc3101 Human nov  
Ade4296 Human MIC  
Abm8235 Tumour-as  
Ade48308 Human MIC  
Aam00864 Human bon  
Adc31005 Human nov  
Ham16170 Peptide #

OM protein - protein search, using sw model  
Run on: May 20, 2006, 17:05:37 ; Search time 199 Seconds  
(Without alignments)  
2472.185 Million cell updates/sec

Title: US-09-856-723a-8  
Perfect score: 5489  
Sequence: I MKQYASPMPTQTDVKLKFKP.....RTLEQNKGKMAKKKEKCVLQ 1076

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext: 0.5  
Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*

1: geneseqp1980:,\*  
2: geneseqp1990s:,\*  
3: geneseqp2008s:,\*  
4: geneseqp2001:,\*  
5: geneseqp2002s:,\*  
6: geneseqp2003as:,\*  
7: geneseqp2003bs:,\*  
8: geneseqp2004s:,\*  
9: geneseqp2005s:,\*  
10: geneseqp2006s:,\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query % Match Length DB ID

Description

#### ALIGNMENTS

RESULT	1
ID	AAU74355
XX	AAU74355 standard; protein; 1076 AA.
XX	AAU74355;
XX	DT 12-MAR-2002 (first entry)
XX	Human cytoskeleton-associated protein (CYSKE) #26.
XX	Human; cytoskeleton-associated protein; CYSKE; autoimmune disorder; cell proliferation disorder; inflammatory disorder; prion disease; vehicle trafficking disorder; gastrointestinal disorder; muscle disorder; neurological disorder; cell motility disorder; reproductive disorder; spinal cord disease; central nervous system disorder; mental disorder; gene therapy; cancer.
XX	KW
OS	Homo sapiens.
XX	
FN	WO200185942-A2.
XX	
PD	15-NOV-2001.
XX	
PR	03-MAY-2001; 2001WO-US014355.
XX	
PR	05-MAY-2000; 2000US-0201960P.
PR	05-JUN-2000; 2000US-0209705P.
PR	07-JUN-2000; 2000US-0210149P.
PR	21-JUN-2000; 2000US-0213215P.
XX	
PA	(INCY-) INCYTE GENOMICS INC.
XX	
PI	Yue H, Tang YT, Au-Young J, Lu DAM, Baughn MR, Hillman JL, Kearney L, Azimzai Y, Lal P, Yao MG, Bandman O, Burford N, Batra S,
PI	Aam9322 Human pol
PI	Abg22882 Novel hum
PI	Adj0136 Human hea
DR	Abg22882 Novel hum
DR	Abg22882 Novel hum
XX	
PT	Yay51415 Human wil
PT	Aay51417 Human pke
PT	Aam8789 Human pro
PT	Aay51416 Human pke
PT	Abg22880 Novel hum
PT	Abg22882 Drosophil
PT	Aab92539 Human pro

Claim 1; Page 153-155; 194pp; English.

xx  
 CC The invention relates to human cytoskeleton-associated polypeptides (CYSKP) and their associated polynucleotide sequences. The sequences are useful in the treatment of disorders associated with overexpression or underexpression of CYSKP in a patient. The disorders include cell proliferative disorders (such as cancer, actinic keratosis, acterioclerosis, cirrhosis, hepatitis and psoriasis), autoimmune/inflammatory disorders (such as, asthma, atherosclerosis, osteoporosis, Crohn's disease, rheumatoid arthritis, diabetes mellitus and anemia), vesicle trafficking disorders (such as hypercholesterolemia, diabetes insipidus, Graves' disease and goitre), gastrointestinal disorders, priion diseases, neurological disorders (such as epilepsy, stroke, cerebral neoplasma, Alzheimer's disease, Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis and other motor neuron disorders), cell motility disorders, reproductive disorders (such as endometriosis and polycystic ovary syndrome), muscle disorders (such as myoclonus, migraine, hypertension, hypoglycaemia, myocardial infarction, epilepsy and muscular dystrophy), spinal cord diseases, central nervous system disorders (such as Down syndrome and cerebral palsy) and mental disorders (such as anxiety and schizophrenia).  
 CC Sequences AAU74330-AAU74363 represent human CYSKP of the invention  
 xx  
 SQ Sequence 1076 AA;

Query Match 99.9%; Score 5486; DB 5; Length 1076;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 1075; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKQYASPMPTQDVKLKEPKLKVSAALQFSIASCIFURGKATDEMQSLASIVSMQ 60  
 Db 1 MKQYASPMPTQDVKLKEPKLKVSAALQFSIASCIFURGKATDEMQSLASIVSMQ 60  
 QY 61 ADIGNLDDPFEEDNEDDENRDNVQHREKAAKITELINKNLFDAEAKDLATVNNSNPDDDA 120  
 Db 61 ADIGNLDDPFEEDNEDDENRDNVQHREKAAKITELINKNLFDAEAKDLATVNNSNPDDDA 120  
 QY 121 AKANPFGPDSSEPIETASPRKTEDSFYNNSNPKEVOTPOYLNPFEPRAFTIKD 180  
 Db 121 AKANPFGPDSSEPIETASPRKTEDSFYNNSNPKEVOTPOYLNPFEPRAFTIKD 180  
 QY 181 PPOSTKRKIRPVDMSKVLYADSSKTEERBLDESNPPFEPKSTPPPNLVNPQBLETR 240  
 Db 181 PPOSTKRKIRPVDMSKVLYADSSKTEERBLDESNPPFEPKSTPPPNLVNPQBLETR 240  
 QY 241 RVKKKAPAPPVLSPTKTVGVLNENTVSGAKDLSTSPKPSFIPSPVPLGRKENASQLLWCKE 300  
 Db 241 RVKKKAPAPPVLSPTKTVGVLNENTVSGAKDLSTSPKPSFIPSPVPLGRKENASQLLWCKE 300  
 QY 301 VTKNYRGVQLTNTFTSWRNGLSCAIIHFRPDLDYKSLNPODIKENNKAVDGASIG 360  
 Db 301 VTKNYRGVQLTNTFTSWRNGLSCAIIHFRPDLDYKSLNPODIKENNKAVDGASIG 360  
 QY 361 ISRLLEPSDMVLLAIPDKLTWMTLYQIRAHPSQELNVQIEENNSKTYKIGNYDT 420  
 Db 361 ISRLLEPSDMVLLAIPDKLTWMTLYQIRAHPSQELNVQIEENNSKTYKIGNYDT 420  
 QY 421 NSSVDOQEKEYAELSDLRKBPPEOOGISAVDPLSODDSVPVNDSGVGSESESHTOPDHL 480  
 Db 421 NSSVDOQEKEYAELSDLRKBPPEOOGISAVDPLSODDSVPVNDSGVGSESESHTOPDHL 480  
 QY 481 SOSTASPICRTKSDTEPKSOSSGRSGSDDPGCINTSDTOAQVILGKRKLKARTL 540  
 Db 481 SOSTASPICRTKSDTEPKSOSSGRSGSDDPGCINTSDTOAQVILGKRKLKARTL 540  
 QY 541 ELSLDYVSDKKKOMSPRPICEBDQKQTLIDGSNLKEKLNRSLECRSPESPPIK 600  
 Db 541 ELSLDYVSDKKKOMSPRPICEBDQKQTLIDGSNLKEKLNRSLECRSPESPPIK 600  
 QY 601 TSISPTSKLGYS'SRDLIAKKGHASLROTESDADRTLNADHSKIVQWRLLSRQE 660  
 Db 601 TSISPTSKLGYS'SRDLIAKKGHASLROTESDADRTLNADHSKIVQWRLLSRQE 660  
 QY 661 ELKERARVILLEQARRDAALKAGNKHNTNTATPCNCNQLSDQODBERRQLRERQIATAE 720

Db 61 ELKERARVILLEQARRDAALKAGNKHNTNTATPCNCNQLSDQODBERRQLRERQIATAE 720  
 QY 721 ARSGYKMSLPSGEMABKLKERSKAGSDENIDEITNEPEGFWGGGBLNTEN 780  
 Db 721 ARSGYKMSLPSGEMABKLKERSKAGSDENIDEITNEPEGFWGGGBLNTEN 780  
 QY 781 DLDTPBQNSKLVDLKUKLEVOPOVANISPSSAAQAVYTESSEQDMKGCTEDLTERIQLK 840  
 Db 781 DLDTPBQNSKLVDLKUKLEVOPOVANISPSSAAQAVYTESSEQDMKGCTEDLTERIQLK 840  
 QY 841 TTEPRNPVUFSKDSTVRKTOLESFSQYJENRPMKRSIQDTCKKNEEKAIETQR 900  
 Db 841 TTEPRNPVUFSKDSTVRKTOLESFSQYJENRPMKRSIQDTCKKNEEKAIETQR 900  
 QY 901 KPSDEBVNLKGKDTSQTYVGBALENEQKQDTRAALKVRLYMDGRATEEAM 960  
 Db 901 KPSDEBVNLKGKDTSQTYVGBALENEQKQDTRAALKVRLYMDGRATEEAM 960  
 QY 961 MQBNFMLANKNALLRNMOLSLKEKDLRVEYLARELMLAEDWQKTAQKRE 1020  
 Db 961 MQBNFMLANKNALLRNMOLSLKEKDLRVEYLARELMLAEDWQKTAQKRE 1020  
 QY 1021 OLLIDELVALVNKGDALYRDIDQEQKFEEDBHLERTLEONIKGKMKRBEKCVLQ 1076  
 Db 1021 OLLIDELVALVNKGDALYRDIDQEQKFEEDBHLERTLEONIKGKMKRBEKCVLQ 1076

#### RESULT 2

ID ADL13160 Standard; protein; 1076 AA.  
 XX ADL13160;  
 AC XX  
 DT 06-MAY-2004 (first entry)

DB Human steroid-induced C3A liver cell protein #134.  
 KW Hepatotropic; Gene therapy; Wilson disease; liver disorder;  
 KW steroid therapy; cirrhosis; hepatitis; human; C3A liver cell.  
 KW Homo sapiens.

XK PN US6673549-B1.  
 XK PR 06-JAN-2004.  
 XK PA (INCY-) INCYME CORP.  
 XK PI 12-OCT-2001, 2001US-00976594.  
 XK DR 12-OCT-2000, 2000US-0240409P.

XK Disclosure; SEQ ID NO 889; 141pp; English.

XK PT Combination useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis, comprises cDNA that are differentially expressed in response to steroid treatment.  
 XK Disclosure; SEQ ID NO 889; 141pp; English.

CC The invention relates to a combination comprising cDNAs that are differentially expressed in response to steroid treatment. Also included are the following: a high throughput method for using a cDNA to detect differential expression of nucleic acids in a sample; and a high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA. The sample is from a subject with Wilson disease and comparison of a standard defines a stage of that disease. The high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA comprises: combining

CC the combination with molecules or compounds under conditions to allow  
 CC specific binding; and detecting specific binding between each cDNA and at  
 CC least one molecule or compound. The molecules or compounds are regulatory  
 CC proteins. The combination is useful for preparing a composition for  
 CC treating liver disorders associated with steroid therapy, e.g., cirrhosis  
 CC or hepatitis. The present sequence represents a human protein which is  
 CC differentially expressed in steroid-induced C3A liver cells. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format directly from USPO  
 CC at seqdata.uspo.gov/sequence.html.

xx

Sequence 1076 AA;

Query Match 99.9%; Score 5486; DB 8; Length 1076;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1075; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKQVQASPMPTOTDVKUKPKPSKVKVVAALQFSLSCLIFLAKGKATTDMSOLASLVSMKQ 60

Db 1 MKQVQASPMPTOTDVKUKPKPSKVKVVAALQFSLSCLIFLAKGKATTDMSOLASLVSMKQ 60

Qy 61 ADIGMUDPFDDEDDENRDKNQEBKAKTDLINKFLDAAQDLATINSNPDDPA 120

Db 61 ADIGMUDPFDDEDDENRDKNQEBKAKTDLINKFLDAAQDLATINSNPDDPA 120

Qy 181 PPOSTRKRNTRPVDSKYLADSSKTREREDIDESPPYPBKSTPPENNLPVQLETER 240

Db 181 PPOSTRKRNTRPVDSKYLADSSKTREREDIDESPPYPBKSTPPENNLPVQLETER 240

Qy 241 RYKRKAPAPPYLSPKGVLVENTVSGKDLSTSPPSISPPVPLGRKPNASQSLWCKE 300

Db 241 RYKRKAPAPPYLSPKGVLVENTVSGKDLSTSPPSISPPVPLGRKPNASQSLWCKE 300

Qy 301 VTKNYTRGVKLTNTFTSWRNGISFCATLHHRPDLIDYKSJNPQD1KENNKAYDGAFASIG 360

Db 301 VTKNYTRGVKLTNTFTSWRNGISFCATLHHRPDLIDYKSJNPQD1KENNKAYDGAFASIG 360

Qy 361 ISRLILRPSDMVTLAIPDKLTWTMYLQIRAHPSGOBLVNVQIEBNSKSTYKVGNYDT 420

Db 361 ISRLILRPSDMVTLAIPDKLTWTMYLQIRAHPSGOBLVNVQIEBNSKSTYKVGNYDT 420

Qy 421 NSSVQDKFVAKLSLQKREPLQLOPIGAVDPLSDSVFVNDSGCGESSESHQPDHL 480

Db 421 NSSVQDKFVAKLSLQKREPLQLOPIGAVDPLSDSVFVNDSGCGESSESHQPDHL 480

Qy 481 SPSTASPYCRTTSKSDTEPOQKQSQQSGRTSGSDDPGTCNSTDSTOQVLLGKRLKAETL 540

Db 481 SPSTASPYCRTTSKSDTEPOQKQSQQSGRTSGSDDPGTCNSTDSTOQVLLGKRLKAETL 540

Qy 541 ELSDXVSKDKDMPPRPERERTSDQLOPDIGENLKEKLRSLGCRSPERSPIK 600

Db 541 ELSDXVSKDKDMPPRPERERTSDQLOPDIGENLKEKLRSLGCRSPERSPIK 600

Qy 601 TSLSPTKLAGYSYSDLAQKHSRQLQPSDPAERTTIAHADHSKKVWHRLSRQE 660

Db 601 TSLSPTKLAGYSYSDLAQKHSRQLQPSDPAERTTIAHADHSKKVWHRLSRQE 660

Qy 661 ELSKERARVLLQARRODAALKAGKKGKNTNTTPCNCRQLSDQDERRQLRQLAB 720

Db 661 ELSKERARVLLQARRODAALKAGKKGKNTNTTPCNCRQLSDQDERRQLRQLAB 720

Qy 721 ARSGYNSLEPSYGENAAKLRKASGENDNTRIDTNERIPIGSFVGGEDELNLN 780

Db 721 ARSGYNSLEPSYGENAAKLRKASGENDNTRIDTNERIPIGSFVGGEDELNLN 780

Qy 781 DLDTPRQNSKVLQDALKKLGKLEQVQVANSSSAACKAVNTTFFCNQRLSDQDERRQLRQLAB 840

Db 781 DLDTPRQNSKVLQDALKKLGKLEQVQVANSSSAACKAVNTTFFCNQRLSDQDERRQLRQLAB 840

SQ Sequence 1231 AA;

QY

841 TTERFPNVPSKOSTVRKQLOSSQSIERNPEMKRQSQTQDTKGNGNEKAATTOR 900

Db 841 TTERFPNVPSKOSTVRKQLOSSQSIERNPEMKRQSQTQDTKGNGNEKAATTOR 900

QY 901 KPSEDEVLNKGFKDTSQVYVGLAALNEOKQDITRAVLYKRYIMDGTQRNTBEEAM 960

Db 901 KPSEDEVLNKGFKDTSQVYVGLAALNEOKQDITRAVLYKRYIMDGTQRNTBEEAM 960

QY 961 MOBWFMLVNUKNGNALLRRMNOLSLRERHDLLERYZLLNRBLRAMLAEDWQTEAQRR 1020

Db 961 MOBWFMLVNUKNGNALLRRMNOLSLRERHDLLERYZLLNRBLRAMLAEDWQTEAQRR 1020

QY

1021 QLIDDBLVALVNUKRALVRLDAQEKOAEDEHLLERTLONKGMAKKERCVLQ 1076

Db 1021 QLIDDBLVALVNUKRALVRLDAQEKOAEDEHLLERTLONKGMAKKERCVLQ 1076

QY

1021 QLIDDBLVALVNUKRALVRLDAQEKOAEDEHLLERTLONKGMAKKERCVLQ 1076

Db

RESULT 3

ADX07701

ID ADX07701 standard; protein; 1231 AA.

XX

AC ADX07701;

XX

DT 21-APR-2005 (first entry)

XX

DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 2266.

XX

KW cytostatic; cyclin-dependent kinase; cdk; biomarker.

XX

OS Homo sapiens.

XX

FN WO2005012875-A2.

XX

FR 29-JUL-2003; 2003US-0490890P.

XX

PD 10-FEB-2005.

XX

PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX

PI Li, M., Rupnow BA., Webster KR., Jackson DG., Wong TW;

XX

DR WPI; 2005-163068/17.

DR N-PSDB; ADX07700.

XX

PT Biomarkers useful for predicting or determining the response of a mammal to a cancer treatment comprising administration of a modulator of cyclin-dependent kinase activity.

XX

PS Claim 5; SEQ ID NO 2266; 141pp; English.

XX

CC This invention describes a novel method of predicting or determining whether a mammal will respond or is responding to an anti-cancer agent that modulates cyclin-dependent kinase (cdk) activity. The method comprises measuring the level of one or more biomarkers selected from 274 biomarkers given in the specification (nucleotide sequence SEQ ID NO:1246 (Genbank ESR W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether a patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify biomarkers. The cdk modulator is preferably N-(5-(1,1-dimethylethyl)-2-oxazolylmethylthio]-2-thiophenyl-4-piperidine carboxamide, 0.5-L-tartric acid salt. Note: The sequence data for this pattern did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published\_pct\_sequences. This sequence represents a biomarker used in the method of the invention.

XX

Sequence 1231 AA;

Query Match	99.2%	Score	5442.5	DB	9	length	1231		
Best Local Similarity	96.6%	Pred.	No. 0						
Matches	1073	Conservative	1	Mismatches	2	Indels	35	Gaps	1
Qy	1	MKQYASPMPTOTDVKLKFPLSKVVAALQFLSLCIFLRKGATDEDMOSLASIVSMQ	60						
Db	121	MKQYASPMPTOTDVKLKFPLSKVVAALQFLSLCIFLRKGATDEDMOSLASIVSMQ	60						
Qy	61	ADIGNLDIFEDNDDDEWRVNOERAAKIT.....	91						
Db	181	ADIGNLDIFEDNDDDEWRVNOERAAKIT.....	91						
Qy	92	-----ELINKLNLTDAEKDLATNSNPFPDPDAEINPFGGDSEBEPITETASPRKE	145						
Db	241	SASSBEBLINKNLVEAKDLATNSNPFPDPDAEINPFGGDSEBEPITETASPRKE	145						
Qy	146	DSFTYNSTNPFPKEYQTPOYINPPDEPEARTVTKIUSPPOSTKRKNIRPVMSKVLYADSK	205						
Db	301	DSFTYNSTNPFPKEYQTPOYINPPDEPEARTVTKIUSPPOSTKRKNIRPVMSKVLYADSK	205						
Qy	205	TERHELDSSNPFPYRKSTPPNNLVNPQELETERRVRKAAPVPLSPTGVILVENTUS	265						
Db	361	TERHELDSSNPFPYRKSTPPNNLVNPQELETERRVRKAAPVPLSPTGVILVENTUS	265						
Qy	481	IUHFRPDIDYKSLNPODIKENKKAYDGFASIGISRLIPSDMVLLAIPDKLTWMTL	540						
Db	386	YQIRAHFSGOBELNTVOIBERNSSKSYKVNGTETUNSSDQEYAEELSKEPELLOOP	445						
Qy	541	YQIRAHFSGOBELNTVOIBERNSSKSYKVNGTETUNSSDQEYAEELSKEPELLOOP	600						
Db	446	ISGAVDPLSQDPSVNDGVGESSESERHQTPDHLSPTASPKCRTKSDTEPKQSQSS	505						
Qy	601	ISGAVDPLSQDPSVNDGVGESSESERHQTPDHLSPTASPKCRTKSDTEPKQSQSS	660						
Db	506	GRYSGSGDDGGICCSNMDSTOARQVILGKRRLLKAETLBSLDSLYVSDRKKKOMSPPTCEETDE	565						
Qy	661	GRYSGSGDDGGICCSNMDSTOARQVILGKRRLLKAETLBSLDSLYVSDRKKKOMSPPTCEETDE	720						
Db	566	QKLQTLDGGSNLLEGEKLENSRSLCRSDPESPIKTSASPTSKLGYSRSRDLLAKKHA	625						
Qy	721	QKLQTLDGGSNLLEGEKLENSRSLCRSDPESPIKTSASPTSKLGYSRSRDLLAKKHA	780						
Db	626	SIROTESPDADRTLNHADHSSKVHORLLSROBELKERARVILBOARDRAKAGNKH	685						
Qy	781	SIROTESPDADRTLNHADHSSKVHORLLSROBELKERARVILBOARDRAKAGNKH	840						
Db	686	NTNTATPFCNRQLSDQDQBERRQLRERARQLTAEARSGVMSKELPSYGMMAEKLERS	745						
Qy	841	NTNTATPFCNRQLSDQDQBERRQLRERARQLTAEARSGVMSKELPSYGMMAEKLERS	900						
Db	746	KASGDENNIEIDTNEPERPEGFVGGDALTNLENDLDPENSKVLUKLKLULEVOPQ	805						
Qy	901	KASGDENNIEIDTNEPERPEGFVGGDALTNLENDLDPENSKVLUKLKLULEVOPQ	960						
Db	806	VANSPSSAQAKTETESSEODMKSCTEDLARTELOKTERPRNPVFSKOSTVRKTOLSP	865						
Qy	961	VANSPSSAQAKTETESSEODMKSCTEDLARTELOKTERPRNPVFSKOSTVRKTOLSP	1020						
Db	866	SQTENRDEMOKRQSIQDENTKKGMEKAIAITETORKPSDEVENKGFKDTSQVNGELAA	925						
Qy	1021	SQTENRDEMOKRQSIQDENTKKGMEKAIAITETORKPSDEVENKGFKDTSQVNGELAA	1080						
Db	926	LENBOKOIDTRALVEKURLYLMGTGRNTEERAMMQWFMUNKKNKLIRNMOLSLIE	985						
Qy	1081	LENBOKOIDTRALVEKURLYLMGTGRNTEERAMMQWFMUNKKNKLIRNMOLSLIE	1140						
Qy	986	KEHDLERVELLERLMLAIDWQKTAQRBLQDDELVALVNGRDALVRDQF	1045						
Db	1141	KEHDLERVELLERLMLAIDWQKTAQRBLQDDELVALVNGRDALVRDQF	1200						
Qy	1046	KOABEBDEBLERTEQNKGKMKKEBECKULQ	1076						
Db	1201	KOABEBDEBLERTEQNKGKMKKEBECKULQ	1231						
Qy	904	RESULT 4							
Db	1201	ADSL15640 standard: protein; 1040 AA.							
XX	ADSL15640;								
XX	AC								
XX	DT	29-JAN-2004 (first entry)							
XX	DE	Human structural and cytoskeleton-associated protein (SCAP) #19.							
XX	DE	Human structural and cytoskeleton-associated protein; SCAP; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; myelofibrosis; psoriasis; cancer; pneumonia; chronic bronchitis; yellow fever; influenza; measles; mumps; HIV; human T lymphotropic virus; rabies; cerebral palsy; encephalitis; rubella; epilepsy; ischaemic cerebrovascular disease; stroke; cerebral neoplasm; Alzheimer's disease; Pick's disease; Huntington's disease; dementia; hereditary ataxia; multiple sclerosis; meningitis; brain abscess; pripon disease; Creutzfeldt-Jakob disease; insomnia; neurofibromatosis; cerebral palsy; myasthenia gravis; anxiety.							
XX	OS	Homo sapiens.							
XX	PN	W02003062391-A2.							
XX	PD	31-JUL-2003.							
XX	PF	16-JAN-2003; 2003W0-US001772.							
XX	PR	18-JAN-2002; 2002US-0350702P.							
PR	25-JAN-2002; 2002US-0351715P.								
PR	12-FEB-2002; 2002US-0357402P.								
PR	10-MAY-2002; 2002US-0379880P.								
PR	17-MAY-2002; 2002US-0381593P.								
PR	07-JUN-2002; 2002US-0387270P.								
PR	19-JUL-2002; 2002US-0397128P.								
XX	PA	(INCY-) INCYTE GENOMICS INC.							
XX	PT	Yue H, Griffin JR, Richardson TW, Tang YT, Thangavelu K; Forbyte IJ, Beeha SD, Chawla NK, Hafalia A, Swarnkar A; Marquis JP, Gorvad AB, Baughn MR, Lu DM, Arvizu CS, Kable AE; Lee SY, Ramkumar J, Jiang X, Jackson AA, Khare R, Elliott VS; Bulloch SA, Xu Y, Lee S, Lehr-Mason PM; XX DR; WPI; 2003-671468/63.							
XX	PS	Claim 1; SEQ ID NO 19; 357pp; English.							
CC	The invention comprises the amino acid and coding sequences of human structural and cytoskeleton-associated protein (SCAP). The SCAP DNA and protein sequences of the invention are useful for the diagnosis and treatment of: arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, myelofibrosis, psoriasis, primary cancer, pneumonia, chronic bronchitis, yellow fever, influenza, measles, mumps, HIV, human T lymphotropic virus, rabies, gastroenteritis, encephalitis, rubella, epilepsy, ischaemic cerebral disease, stroke, cerebral neoplasm, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, hereditary ataxia, multiple sclerosis, meningitis, brain abscess, pripon disease, Creutzfeldt-Jakob disease, insomnia, neurofibromatosis, cerebral palsy; myasthenia gravis; anxiety.								

CC sclerosis, meningitis, brain abscess, prion disease, Creutzfeldt-Jakob  
 CC disease, insomnia, neurofibromatosis, cerebral palsy, myasthenia gravis,  
 CC anxiety. The present amino acid sequence represents a human SCAP of the  
 CC invention.

SQ Sequence 1040 AA:

```

Query Match 95.9%; Score 5266; DB 7; Length 1040;
Best Local Similarity 96.6%; Pred. No. 2.8e-316;
Matches 1039; Conservative 1; Mismatches 0; Indels 36; Gaps 1;
OQ
  1 MKQYASPMPTDVKLKKPKPSKVVSAALQPSLSCIPLRKGKATDEMDQSLASLVSMSQ 60
  1 MKQYASPMPTDVKLKKPKPSKVVSAALQPSLSCIPLRKGKATDEMDQSLASLVSMSQ 60
  61 ADIGNDDPFDNEDDENRNRNQEAKATKLINKLNPLDAAKDLATWSNPDDPA 120
  61 ADIGNDDPFDNEDDENRNRNQEAKATKLINKLNPLDAAKDLATWSNPDDPA 120
  61 ADIGNDDPFDNEDDENRNRNQEAKATKLINKLNPLDAAKDLATWSNPDDPA 120
  121 ARLNPGDPDSEEPETETASRKTEPSYNNSYNPPREVQVTOYLNPPDREAFVTKDS 180
  121 ARLNPGDPDSEEPETETASRKTEPSYNNSYNPPREVQVTOYLNPPDREAFVTKDS 180
  181 PPOSTERKNITFVDMKYLMDSSKTERBEDIDESNFYPPEPSTPPPNLYNPVQLETER 240
  181 PPOSTERKNITFVDMKYLMDSSKTERBEDIDESNFYPPEPSTPPPNLYNPVQLETER 240
  241 RYVKRKAAPPPLSPKGVLNTVSAGKDLTSKPSPISSVLUGRKPNASQSLWCKE 300
  241 RYVKRKAAPPPLSPKGVLNTVSAGKDLTSKPSPISSVLUGRKPNASQSLWCKE 300
  301 VTKNYRGVKINTFTSWRNGISFCATLHHFRPDLDIYKSJNPQDIKENNKAYDGASIG 360
  301 VTKNYRGVKINTFTSWRNGISFCATLHHFRPDLDIYKSJNPQDIKENNKAYDGASIG 360
  361 ISRLLEPSPDMVLLAFLDKLTWNTYLIQIRAFRSQGOBLNVYQIBENSKSTKVGNYETDT 420
  361 ISRLLEPSPDMVLLAFLDKLTWNTYLIQIRAFRSQGOBLNVYQIBENSKSTKVGNYETDT 420
  421 NSSVQDKFVNLSDKREPLQQLQPIGAVDPLQSDSVDFTSGVGESESHEQPDH 480
  421 NSSVQDKFVNLSDKREPLQQLQPIGAVDPLQSDSVDFTSGVGESESHEQPDH 480
  421 NSSVQDKFVNLSDKREPLQQLQPIGAVDPLQSDSVDFTSGVGESESHEQPDH 480
  481 SPSTASPYCRTKSIDTEPOQKQQSSGRTSGSDDPGICSNNTDSTQAVLIGKRLKAETL 540
  481 SPSTASPYCRTKSIDTEPOQKQQSSGRTSGSDDPGICSNNTDSTQAVLIGKRLKAETL 540
  541 ELSLDIVSKDKDMPPFPIERBTDSOKLQDINGSLNEKLERGLNSRLBRSPESPIK 600
  541 ELSLDIVSKDKDMPPFPIERBTDSOKLQDINGSLNEKLERGLNSRLBRSPESPIK 600
  601 TSLSPTKUGSYSRDLAKKKHSRLQTESPDADRTTINAHDSKQVHRLRSQ 660
  601 TSLSPTKUGSYSRDLAKKKHSRLQTESPDADRTTINAHDSKQVHRLRSQ 660
  661 ELSKERAVLILQARRDALKGKRNNTATPPCIRQLSDQOERRRLERAROLAE 720
  661 ELSKERAVLILQARRDALKGKRNNTATPPCIRQLSDQOERRRLERAROLAE 720
  721 ARSGVMSLPSYGENMAEKERSKASGBENDTBIDTBEIPEGFWVGCGDELNLN 780
  721 ARSGVMSLPSYGENMAEKERSKASGBENDTBIDTBEIPEGFWVGCGDELNLN 780
  721 ARSGVMSLPSYGENMAEKERSKASGBENDTBIDTBEIPEGFWVGCGDELNLN 780
  721 ARSGVMSLPSYGENMAEKERSKASGBENDTBIDTBEIPEGFWVGCGDELNLN 780
  781 DLDTPRQNSKVKDCLKKLLVEQPOVANSSSAAQKAVTESSEOMKSCEDTLERLOK 840
  781 DLDTPRQNSKVKDCLKKLLVEQPOVANSSSAAQKAVTESSEOMKSCEDTLERLOK 840
  750 - - - BONSKLVDKLUKLVEQPOVANSSSAAQKAVTESSEOMKSCEDTLERLOK 804
  841 TERFRNPVVFSEKDKSTVKTQLOSQYIERPEMKRQSIQEDTKGNKEAKATTOR 900
  805 TTERFRNPVVFSEKDKSTVKTQLOSQYIERPEMKRQSIQEDTKGNKEAKATTOR 864
  901 KPSDEBVNLKQKDKTQSYYVGLAALENKEQDITRAVLYERLRLYMDTGNTTREBAM 960
  
```

Db 865 KPSDEBVNLKQKDKTQSYYVGLAALENKEQDITRAVLYERLRLYMDTGNTTREBAM 924
 QY 961 MOBWFMLVNKNALIRRNMNOLSLRERLERYSELNLREMLAIEDMOTKEQRRE 1020
 Db 925 MQEWFMVLVNKNALIRRNMNOLSLRERLERYSELNLREMLAIEDMOTKEQRRE 984

Db 1021 QLLDRVALVNRDALVLDQESKQAESEDEHLERTLEONKGMAKKEKCVLQ 1076
 QY 985 QLLDRVALVNRDALVLDQESKQAESEDEHLERTLSQNKGMAKKEKCVLQ 1040

R5ULT 5
 AM7878
 ID AAM78788 standard; protein; 1581 AA.
 XQ
 AC AAM78788;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 1450.
 XX
 PP
 XQ
 Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 nervous system disorder; arthritis; inflammation.
 OS Homo sapiens.
 XX
 BN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PP 05-FEB-2001; 2001WO-US00498.
 XQ
 PR 03-FEB-2000; 2000US-00436914.
 PR 27-APR-2000; 2000US-00530875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00630325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00653561.
 PR 20-OCT-2000; 2000US-00633325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 PA (HYSB-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Abundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZN;
 PI Xue AJ, Yang Y, Wejhran T, Goodrich R;
 XX
 DR WPI: 2001-476283/51.
 DR N-PSDB; AAK51921.
 XX
 PR Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PR in diagnosis and gene therapy.
 XX
 PR Claim 20; Page 3716-3718; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAW78323-AAW80320) that exhibit activity relating to
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 e.g. stem cell growth factor activity, haemopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for ID NO 2110 (AAK51581), 2111
 CC (AAK52282) and 3666 (AAW8020) are omitted as the relevant pages from the
 sequence listing were missing at the time of publication
 XX
 Sequence 1581 AA;

Query	Match	94.4%; Score 5183; DB 4; Length 1581;
	Best Local Similarity	67.6%; Pred. No. 6.7e-311;
	Matches	1; Mismatches 0; Indels 512; Gaps 1;
Qy	8	MPTQTDVKFKPLSKKVVSAALQFSLSCIFLRECKATDQMOSLASLYSMQADIGNID
Db	1	MPTQTDVKFKPLSKKVVSAALQFSLSCIFLRECKATDQMOSLASLYSMQADIGNID
Qy	68	DFFEDNEDDBRNRYNOEKKAKITPELKLNPLDEAKDLATVNSPFDPPDAELNPFG
Db	61	DFFEDNEDDBRNRYNOEKKAKITPELKLNPLDEAKDLATVNSPFDPPDAELNPFG
Qy	128	DPSBEPITETASPRKTESPYNNSYNPKEVQTPQYIAPPDEBAFTIKSPSQTTR
Db	121	DPSBEPITETASPRKTESPYNNSYNPKEVQTPQYIAPPDEBAFTIKSPSQTTR
Qy	188	KNIRPVDMKLYADSKTBEELDESBNPYPKSTPPNNLVAPVQELETTERVKRKP
Db	181	KNIRPVDMKLYADSKTBEELDESBNPYPKSTPPNNLVAPVQELETTERVKRKP
Qy	248	APPVLSPKTCGVLENNTVSAGKDLSTSPKSPSPIPSPVILGKPKNASOLLVWCKEVTKNG
Db	241	APPVLSPKTCGVLENNTVSAGKDLSTSPKSPSPIPSPVILGKPKNASOLLVWCKEVTKNG
Qy	308	VKINTNFTSWRNGLSFCATLHFRPDLQYKLMQDENTENKAYDFASIGSRLEP
Db	301	VKINTNFTSWRNGLSFCATLHFRPDLQYKLMQDENTENKAYDFASIGSRLEP
Qy	368	SDMULLALPDKLTVMTLYQI RAHFSGQBLNVOBLENSKSTKVGNBTDTNSVQD
Db	361	SDMULLALPDKLTVMTLYQI RAHFSGQBLNVOBLENSKSTKVGNBTDTNSVQD
Qy	428	KFYAELSDIKREPELQOPISGAUPLSODSDVFTNDGSGESESEHQTPDDHSPSTASP
Db	421	KFYAELSDIKREPELQOPISGAUPLSODSDVFTNDGSGESESEHQTPDDHSPSTASP
Qy	488	YCRRTKSDTEPQESQSSRTSSDDPGCNSNTSTOQAVLIGKRLKAETLBDLV
Db	481	YCRRTKSDTEPQESQSSRTSSDDPGCNSNTSTOQAVLIGKRLKAETLBDLV
Qy	548	SDKKKDMSPPICTEDEQKLQTDIGSNLKEKCLNSRSLECRSPSPKIKLSTS
Db	541	SDKKKDMSPPICTEDEQKLQTDIGSNLKEKCLNSRSLECRSPSPKIKLSTS
Qy	608	KLGYSYRSLDACKKHSRLQTESDPADRTLHADISSKTVORHLISRQRLKERRQ
Db	601	KLGYSYRSLDACKKHSRLQTESDPADRTLHADISSKTVORHLISRQRLKERRQ
Qy	668	VLUFOARDAALAKAGNKENTTATPFCNQLSDQDEERRQRERAMOLIASRGYTN
Db	651	VLUFOARDAALAKAGNKENTTATPFCNQLSDQDEERRQRERAMOLIASRGYTN
Qy	728	SEPSYGMAAEKLKERSKGASDENDNIRIDTNEKIPCGFVGGDELTNLEUDLPEQ
Db	721	SEPSYGMAAEKLKERSKGASDENDNIRIDTNEKIPCGFVGGDELTNLEUDLPEQ
Qy	788	NSLKVLVDLKLKCLAEVPOVANSSSAQAKAVTSESEQDKGTFDLTRBKTYTERFRN
Db	781	NSLKVLVDLKLKCLAEVPOVANSSSAQAKAVTSESEQDKGTFDLTRBKTYTERFRN
Qy	848	PVVFSKOSTVRKTOLOSOQIENPEMRORSIQEDTCKRGENERAATETORKPSDEV
Db	841	PVVFSKOSTVRKTOLOSOQIENPEMRORSIQEDTCKRGENERAATETORKPSDEV
Qy	908	LNGCPKOTSQYVGBLALENEQKOIDTRALVEKRLYLMDCRANTEREMAQEWML
Db	901	LNGCPKOTSQYVGBLALENEQKOIDTRALVEKRLYLMDCRANTEREMAQEWML
Qy	968	VNKGNALTRMMNQLSLIKEKHDLERRYELLNR-----
Db	961	VNKGNALTRMMNQLSLIKEKHDLERRYELLNR-----
Qy	1000	-
RESULT 6		
	AMM79773	AMM79773 standard; protein; 1023 AA.
	XX	
	AC	AMM79773;
	XX	
	DT	06-NOV-2001 (first entry)
	XX	
	DE	Human protein SEQ ID NO 3419.
	XX	
	KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haemotopesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
	XX	
	OS	Homo sapiens.
	XX	
	PN	W0200157190-A2.
	XX	
	PD	09-AUG-2001.
	XX	
	PF	05-FEB-2001; 2001WO-US004098.
	XX	
	PR	03-FEB-2000; 2000US-00496914.
	PR	27-APR-2000; 2000US-00560875.
	PR	27-JUN-2000; 2000US-00598075.
	PR	19-JUN-2000; 2000US-0062025.
	PR	01-SEP-2000; 2000US-00654916.
	PR	15-SEP-2000; 2000US-00663561.
	PR	20-OCT-2000; 2000US-00691325.
	PR	30-NOV-2000; 2000US-00728422.
	XX	(HYSE-) HYSEQ INC.
	PA	

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y; Wang D, Wang J, Ren F, Chen R, Wang ZW; PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; PI Xue AJ, Yang Y, Wejhrman T, Goodrich R; DR WPI; 2001-47283/51.

DR N-PSDB; AAK52906.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.

XX Claim 20; Page 328-329; 6221PP; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAK78322-AAK0302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematoopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK5281), 2111 (AAK5282) and 3666 (AAM0020) are omitted as the relevant Pages from the sequence listing were missing at the time of publication

CC (AAK5282) and 3666 (AAM0020) are omitted as the relevant Pages from the sequence listing were missing at the time of publication

CC Sequence 1023 AA;

Query Match Best Local Similarity 94.2%; Score 5173; DB 4; Length 1023; Matches 1011; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 63 IGNLDPEEDNEDDENRVQWEEKAKITELINKNPLDEKEKDLATVNNSPPDDPAE 122

Db 10 LANLDPDEEDNEDDENRVQWEEKAKITELINKNPLDEKEKDLATVNNSPPDDPAE 69

QY 123 IAPFGDPDSEPRITETASPRITEDSFYNNISNPKEVQTPQYLNPFDEPEAFVTIKDSSP 182

Db 70 LNPFGDPDSEPRITETASPRITEDSFYNNISNPKEVQTPQYLNPFDEPEAFVTIKDSSP 129

QY 183 OSTKRKNIRTPDMSKTYLAISSKTTRBEBLRSNPFPYEPKSTTPPNLNUPTQBLTERRY 242

Db 130 OSTKRKNIRTPDMSKLYADSSKTRBEBLDSNPFPYEPKSTTPPNLNUPTQBLTERRY 189

QY 243 KRKAPELLSPKPGVLANENTVSAGDLSTSPKPEPISPVULGRIENASQSSLWCKEV 302

Db 190 KRKAPELLSPKPGVLANENTVSAGDLSTSPKPEPISPVULGRIENASQSSLWCKEV 249

QY 303 KNYRGKIKMTFTSWRNGLSPFCAILHHRFDPLDLYKSLNPKDQIKENKKAYDGASIGIS 362

Db 250 KNYRGKIKMTFTSWRNGLSPFCAILHHRFDPLDLYKSLNPKDQIKENKKAYDGASIGIS 309

QY 363 RLLRPSDMVLLAIPIDKLTWYLYOTRAHFSQGRANWQIENSKSSTYKVGNYETDTS 422

Db 310 RLLRPSDMVLLAIPIDKLTWYLYOTRAHFSQGRANWQIENSKSSTYKVGNYETDTS 369

QY 423 SVDQKKEYARSLDREPELQPIGSADVPLSDQSYFVNDSGVGRSESEHQTDPDHLSP 482

Db 370 SVDQKKEYARSLDREPELQPIGSADVPLSDQSYFVNDSGVGRSESEHQTDPDHLSP 429

QY 483 STASYCCRRTSDTEROKSQOSSGRTGSDDPGLCNTUSTAQNLIGKRRKLKATL 542

Db 430 STASYCCRRTSDTEROKSQOSSGRTGSDDPGLCNTUSTAQNLIGKRRKLKATL 489

QY 543 SDLYSDKKKMSMSPPICTERDEOKLQTLIGSNIERKLRNLSRLCRSDPESPIKTS 602

Db 490 SDLYSDKKKMSMSPPICTERDEOKLQTLIGSNIERKLRNLSRLCRSDPESPIKTS 549

QY 603 LSPTSKLGYSYSDIDLAKKHASLROTESPDADRTTNAHADISKIVORLILSRQEL 662

Db 550 LSPTSKLGYSYSDIDLAKKHASLROTESPDADRTTNAHADISKIVORLILSRQEL 609

QY 663 KERARVILLEQARDAAKAGKHNNTATPCNRQLSDQODBERRQLRERARQLTAR 722

Db 610 KERARVILLEQARDAAKAGKHNNTATPCNRQLSDQODBERRQLRERARQLTAR 669

QY 723 SGVKMSELPSGYEMAELKERSKASGGDENNTIDTNESETPEGFWGGDELNL 782

Db 670 SGVKMSELPSGYEMAELKERSKASGGDENNTIDTNEE1PEGFWGGDELNL 729

QY 783 DTPEONSKLVQKLKLULEVOPQVANSPPSAQAVETESSBQDMKGTEDDLRTERLQTT 842

Db 730 DTPEONSKLVQKLKLULEVOPQVANSPPSAQAVETESSBQDMKGTEDDLRTERLQTT 789

QY 843 ERFRNVVPSKODSTRKTQLOFSQYIENPEMKQRSIQEDTKGNERKAITETQRKP 902

Db 790 ERFRNVVPSKODSTRKTQLOFSQYIENPEMKQRSIQEDTKGNERKAITETQRKP 849

QY 903 SEDBEVNGKGRDSSQYVGIAALENEQKODTRAAVEKRLYAMDGRNTEBERRAMMQ 962

Db 850 SEDBEVNGKGRDSSQYVGIAALENEQKODTRAAVEKRLYAMDGRNTEBERRAMMQ 909

QY 963 BWFMUJNKQALIRPMNQSLLEKHDLLERYELNRLPAMLATEDWQTEACKRERQL 1022

Db 910 EWFMUJNKQALIRPMNQSLLEKHDLLERYELNRLPAMLATEDWQTEACKRERQL 969

QY 1023 LLDBLVALVNGRDALVDAQKQABEDEHLERTLBQNGKROMAKKREKCVLQ 1076

Db 970 LLDBLVALVNGRDALVDAQKQABEDEHLERTLBQNGKROMAKKREKCVLQ 1023

RESULT 7

AMW772

ID AAM79772 standard; protein; 1023 AA.

XX

AC AAM79772;

XX

DT 06-NOV-2001 (first entry)

XX Human protein SEQ ID NO 3418.

DB

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory activity; cancer; leukaemia; nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

XX

PN W0200157190-A2.

XX

PD 09-AUG-2001.

XX

PP 05-FEB-2001; 2001WO-US004098.

XX

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00520325.

PR 01-SEP-2000; 2000US-0054935.

PR 15-SEP-2000; 2000US-00653561.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

PR (HYSB-) HYSBQ INC.

XX

PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y; Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; PI Xue AJ, Yang Y, Wejhrman T, Goodrich R; DR WPI; 2001-47283/51.

DR N-PSDB; AAK52905.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.

PS Claim 20; Page 328; 6221pp; English.  
 XX  
 CC The invention relates to polynucleotides (AAK51456-AAK53415) and the  
 CC encoded polypeptides (AMW823-AMW80302) that exhibit activity elating to  
 cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polymucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 e.g. stem cell growth factor activity, haematoptosis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activity/inhibit activity and may be useful in the diagnosis and/or  
 treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK5381), 2111  
 CC (AMW8232) and 3666 (AMW8020) are omitted as the relevant pages from the  
 CC sequence listing were missing at the time of publication  
 XX Sequence 1023 AA;

Query Match 94.2%; Score 5173; DB 4; Length 1023;  
 Best Local Similarity 99.7%; Pred. No. 1.6e-310; Matches 1023 AA;  
 Matches 1011; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 63 IGNLDDFEEDNEDDENRINQBEKAKitELINKUNFLDEAKOLATVNNSPFDPPDAAR 122  
 Db 10 LANLDDDEEDNEDDENRINQBEKAKitELINKUNFLDEAKOLATVNNSPFDPPDAAR 122  
 QY 123 LNPFGDPDSBEPITETASPRKTEPSPYNNSYNPKEVQTPQYIAMPDPEAFAVMVKDSSP 182  
 Db 70 LNPFQGDPDSBEPITETASPRKTEPSPYNNSYNPKEVQTPQYIAMPDPEAFAVMVKDSSP 129  
 QY 183 QSTKRKNTRPVDMSKYLYADSKTREELDENSBNPFPYERPKSTPPPNLYNPVOELETERV 242  
 Db 130 QSTKRKNTRPVDMSKYLYADSKTREELDENSBNPFPYERPKSTPPPNLYNPVOELETERV 189  
 QY 243 KRKA PAPPVLSPKTCGVLNENTVSAGKDLSTSPKSPSIPPPVPLGKPKPNAQSLLWCKERT 302  
 Db 190 KRKA PAPPVLSPKTCGVLNENTVSAGKDLSTSPKSPSIPPPVPLGKPKPNAQSLLWCKERT 249  
 QY 303 KNYRGVKITNTFTSWRNGLSPCATIAHFRFDDLIYKSLSNPODIKENNKAYDGASIGTS 362  
 Db 250 KNYRGVKITNTFTSWRNGLSPCATIAHFRFDDLIYKSLSNPODIKENNKAYDGASIGTS 309  
 QY 363 RLLRPSDMVLLAIKDGLTMTYQIRAFSGQELNVIOEENSKSTYKVGNETDTS 422  
 Db 310 RLLRPSDMVLLAIKDGLTMTYQIRAFSGQELNVIOEENSKSTYKVGNETDTS 369  
 QY 423 SDVORKPYLELDJKREPQLQPSIGAVDPLSQDSDVFNDSGYGESESEHQPDDHSLP 482  
 Db 370 SDQEEKFYAEELSJKREPQLQPSIGAVDPLSQDSDVFNDSGYGESESEHQPDDHSLP 429  
 QY 483 STASPYCRTCSDTEPKQSSQSSRTSGSDDPGICSNSTDSTQAQVLLGKCRLLKAETBL 542  
 Db 430 STASPYCRTCSDTEPKQSSQSSRTSGSDDPGICSNSTDSTQAQVLLGKCRLLKAETBL 489  
 QY 543 SDLVSKDCKDMSPPFICETBDQKLQTDIGSMLKEKLNRSLECRSDPESPIKTS 602  
 Db 490 SDLVSKDCKDMSPPFICETBDQKLQTDIGSMLKEKLNRSLECRSDPESPIKTS 549  
 QY 603 LSPPSKLGYSYSRDLACKKHSRLQTESPDADRTTIAHADHSKIVVORLISQREL 662  
 Db 550 LSPTSKLGYSYSRDLACKKHSRLQTESPDADRTTIAHADHSKIVVORLISQREL 609  
 QY 663 KERAVLILQARRDAALAKGNKHNTATPPCNOLQDQDDEERRQRERAROLIAZAR 722  
 Db 610 KERAVLILQARRDAALAKGNKHNTATPPCNOLQDQDDEERRQRERAROLIAZAR 669  
 QY 723 SGVNRSEPSYGENMAEKERSKGENDNEDIDTNEIPIGSFGRVGGDELNLNDL 782  
 Db 670 SGVNRSEPSYGENMAEKERSKGENDNEDIDTNEIPIGSFGRVGGDELNLNDL 729  
 QY 783 DTPEQNSKLVLKLUKKLILRVQPOVANSSESAQGVATSESSQDMKSGBDLRLRLOKT 842  
 Db 730 DTPEQNSKLVLKLUKKLILRVQPOVANSSESAQGVATSESSQDMKSGBDLRLRLOKT 789

RESULT 8  
 ABG2283  
 ID ABG2283 standard; protein; 1023 AA.  
 XX  
 AC ABG2283;  
 XX DT 18-FEB-2002 (first entry)  
 XX DB Novel human diagnostic protein #22874.  
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.  
 XX OS Homo sapiens.  
 XX PN WO200115067-A2.  
 XX PD 11-OCT-2001.  
 XX PF 30-MAR-2001; 2001WO-US008631.  
 XX PR 31-MAR-2000; 2000US-00540217.  
 XX DR 23-AUG-2000; 2000US-00649167.  
 XX PA (HYSB-) HYSEQ INC.  
 XX PT Drmanac RT, Liu C, Tang YT;  
 XX DR WPI; 2001-639362/73.  
 XX N-PSDB; AAS81070.  
 XX  
 New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 20; SEQ ID NO 53242; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridization probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 genes. (I) is useful in gene therapy techniques to restore normal  
 activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight marker and as a food  
 supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 amino acid sequences. ABG00010-ABG030377 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)

	Query match	Best local Similarity	Score	DB	Length	Matches	1011; Conservative	2;	Mismatches	11;	Indels	0;	Gaps	0;
b	IGNLDPFEDPENNDDENRNTQEEKAQKATTELINKLNFLDEAKDOLATNSNPFDPPDAE	94.7%	Score 515;	DB 4;	Length 1023;	63	IGNLDPFEDPENNDDENRNTQEEKAQKATTELINKLNFLDEAKDOLATNSNPFDPPDAE	94.7%	Score 515;	DB 4;	Length 1023;	63	IGNLDPFEDPENNDDENRNTQEEKAQKATTELINKLNFLDEAKDOLATNSNPFDPPDAE	94.7%
b	:     LANNJDDEBENDDDENRNTQEEKAQKATTELINKLNFLDEAKDOLATNSNPFDPPDAE	99.7%	Pred. No.	1..6-310;	Length 1023;	10	:     LANNJDDEBENDDDENRNTQEEKAQKATTELINKLNFLDEAKDOLATNSNPFDPPDAE	99.7%	Pred. No.	1..6-310;	Length 1023;	10	:     LANNJDDEBENDDDENRNTQEEKAQKATTELINKLNFLDEAKDOLATNSNPFDPPDAE	99.7%
b	LNPFGDPDPSEBPETASPRKTEDSPYNSYNPKWVQTOXINNPDPBPAFTIKOSSP	123	123	LNPFGDPDPSEBPETASPRKTEDSPYNSYNPKWVQTOXINNPDPBPAFTIKOSSP	182	1.3	LNPFGDPDPSEBPETASPRKTEDSPYNSYNPKWVQTOXINNPDPBPAFTIKOSSP	123	LNPFGDPDPSEBPETASPRKTEDSPYNSYNPKWVQTOXINNPDPBPAFTIKOSSP	182	1.3	LNPFGDPDPSEBPETASPRKTEDSPYNSYNPKWVQTOXINNPDPBPAFTIKOSSP	123	
b	LNPFGDPDSSEPIETASPRKTEDSPYNSYNPKWVQTOXINNPDPBPAFTIKOSSP	70	70	LNPFGDPDSSEPIETASPRKTEDSPYNSYNPKWVQTOXINNPDPBPAFTIKOSSP	129	1.3	LNPFGDPDSSEPIETASPRKTEDSPYNSYNPKWVQTOXINNPDPBPAFTIKOSSP	70	LNPFGDPDSSEPIETASPRKTEDSPYNSYNPKWVQTOXINNPDPBPAFTIKOSSP	129	1.3	LNPFGDPDSSEPIETASPRKTEDSPYNSYNPKWVQTOXINNPDPBPAFTIKOSSP	70	
b	OSTERKNIRPVDMSKYLADSSKTEBEELDESNEPYEPKSTPPNNLNPNVQELETERRV	183	183	OSTERKNIRPVDMSKYLADSSKTEBEELDESNEPYEPKSTPPNNLNPNVQELETERRV	242	2.4	OSTERKNIRPVDMSKYLADSSKTEBEELDESNEPYEPKSTPPNNLNPNVQELETERRV	183	OSTERKNIRPVDMSKYLADSSKTEBEELDESNEPYEPKSTPPNNLNPNVQELETERRV	242	2.4	OSTERKNIRPVDMSKYLADSSKTEBEELDESNEPYEPKSTPPNNLNPNVQELETERRV	183	
b	OSTERKNIRPVDMSKYLADSSKTEBEELDESNEPYEPKSTPPNNLNPNVQELETERRV	130	130	OSTERKNIRPVDMSKYLADSSKTEBEELDESNEPYEPKSTPPNNLNPNVQELETERRV	189	2.4	OSTERKNIRPVDMSKYLADSSKTEBEELDESNEPYEPKSTPPNNLNPNVQELETERRV	130	OSTERKNIRPVDMSKYLADSSKTEBEELDESNEPYEPKSTPPNNLNPNVQELETERRV	189	2.4	OSTERKNIRPVDMSKYLADSSKTEBEELDESNEPYEPKSTPPNNLNPNVQELETERRV	130	
b	KRKAPAPYTLSPKGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	243	243	KRKAPAPYTLSPKGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	302	2.5	KRKAPAPYTLSPKGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	243	KRKAPAPYTLSPKGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	302	2.5	KRKAPAPYTLSPKGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	243	
b	KRKAPAPYTLSPKGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	190	190	KRKAPAPYTLSPKGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	249	2.5	KRKAPAPYTLSPKGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	190	KRKAPAPYTLSPKGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	249	2.5	KRKAPAPYTLSPKGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	190	
b	KKRKPAPVLSPKTGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	303	303	KKRKPAPVLSPKTGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	362	2.5	KKRKPAPVLSPKTGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	303	KKRKPAPVLSPKTGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	362	2.5	KKRKPAPVLSPKTGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	303	
b	KKRKPAPVLSPKTGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	250	250	KKRKPAPVLSPKTGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	309	2.5	KKRKPAPVLSPKTGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	250	KKRKPAPVLSPKTGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	309	2.5	KKRKPAPVLSPKTGVLNENTVSAGKDASTSPKSPISPSPVLPGRKPNAQSLSUWCKRT	250	
b	RLLPSDMVILATEDKLTMTLYQIRAFPSGOBLNVVOIERNNSKSYKVGYETDINS	363	363	RLLPSDMVILATEDKLTMTLYQIRAFPSGOBLNVVOIERNNSKSYKVGYETDINS	422	3.1	RLLPSDMVILATEDKLTMTLYQIRAFPSGOBLNVVOIERNNSKSYKVGYETDINS	363	RLLPSDMVILATEDKLTMTLYQIRAFPSGOBLNVVOIERNNSKSYKVGYETDINS	422	3.1	RLLPSDMVILATEDKLTMTLYQIRAFPSGOBLNVVOIERNNSKSYKVGYETDINS	363	
b	RLLPSDMVILATEDKLTMTLYQIRAFPSGOBLNVVOIERNNSKSYKVGYETDINS	310	310	RLLPSDMVILATEDKLTMTLYQIRAFPSGOBLNVVOIERNNSKSYKVGYETDINS	369	3.1	RLLPSDMVILATEDKLTMTLYQIRAFPSGOBLNVVOIERNNSKSYKVGYETDINS	310	RLLPSDMVILATEDKLTMTLYQIRAFPSGOBLNVVOIERNNSKSYKVGYETDINS	369	3.1	RLLPSDMVILATEDKLTMTLYQIRAFPSGOBLNVVOIERNNSKSYKVGYETDINS	310	
b	SVDOKPKVABSLDKREPELQOPIGSADVPLSDODDSVTFNDSCVGESSEHQOPDDHNSP	423	423	SVDOKPKVABSLDKREPELQOPIGSADVPLSDODDSVTFNDSCVGESSEHQOPDDHNSP	482	3.1	SVDOKPKVABSLDKREPELQOPIGSADVPLSDODDSVTFNDSCVGESSEHQOPDDHNSP	423	SVDOKPKVABSLDKREPELQOPIGSADVPLSDODDSVTFNDSCVGESSEHQOPDDHNSP	482	3.1	SVDOKPKVABSLDKREPELQOPIGSADVPLSDODDSVTFNDSCVGESSEHQOPDDHNSP	423	
b	SVDOKPKVABSLDKREPELQOPIGSADVPLSDODDSVTFNDSCVGESSEHQOPDDHNSP	370	370	SVDOKPKVABSLDKREPELQOPIGSADVPLSDODDSVTFNDSCVGESSEHQOPDDHNSP	429	3.1	SVDOKPKVABSLDKREPELQOPIGSADVPLSDODDSVTFNDSCVGESSEHQOPDDHNSP	370	SVDOKPKVABSLDKREPELQOPIGSADVPLSDODDSVTFNDSCVGESSEHQOPDDHNSP	429	3.1	SVDOKPKVABSLDKREPELQOPIGSADVPLSDODDSVTFNDSCVGESSEHQOPDDHNSP	370	
b	STASPYCRRTKSDTBPQSQOSSGRTSSDDPGICSNJUDSTQAVLICKKRUKIAETEL	483	483	STASPYCRRTKSDTBPQSQOSSGRTSSDDPGICSNJUDSTQAVLICKKRUKIAETEL	542	4.3	STASPYCRRTKSDTBPQSQOSSGRTSSDDPGICSNJUDSTQAVLICKKRUKIAETEL	483	STASPYCRRTKSDTBPQSQOSSGRTSSDDPGICSNJUDSTQAVLICKKRUKIAETEL	542	4.3	STASPYCRRTKSDTBPQSQOSSGRTSSDDPGICSNJUDSTQAVLICKKRUKIAETEL	483	
b	STASPYCRRTKSDTBPQSQOSSGRTSSDDPGICSNJUDSTQAVLICKKRUKIAETEL	430	430	STASPYCRRTKSDTBPQSQOSSGRTSSDDPGICSNJUDSTQAVLICKKRUKIAETEL	489	4.3	STASPYCRRTKSDTBPQSQOSSGRTSSDDPGICSNJUDSTQAVLICKKRUKIAETEL	430	STASPYCRRTKSDTBPQSQOSSGRTSSDDPGICSNJUDSTQAVLICKKRUKIAETEL	489	4.3	STASPYCRRTKSDTBPQSQOSSGRTSSDDPGICSNJUDSTQAVLICKKRUKIAETEL	430	
b	SDIXVSDKCDMSPPFPIEBTDOKGLQTIDIGSNEKEKLENSRLRSBDSPIKTS	543	543	SDIXVSDKCDMSPPFPIEBTDOKGLQTIDIGSNEKEKLENSRLRSBDSPIKTS	602	5.1	SDIXVSDKCDMSPPFPIEBTDOKGLQTIDIGSNEKEKLENSRLRSBDSPIKTS	543	SDIXVSDKCDMSPPFPIEBTDOKGLQTIDIGSNEKEKLENSRLRSBDSPIKTS	602	5.1	SDIXVSDKCDMSPPFPIEBTDOKGLQTIDIGSNEKEKLENSRLRSBDSPIKTS	543	
b	SDIXVSDKCDMSPPFPIEBTDOKGLQTIDIGSNEKEKLENSRLRSBDSPIKTS	490	490	SDIXVSDKCDMSPPFPIEBTDOKGLQTIDIGSNEKEKLENSRLRSBDSPIKTS	549	5.1	SDIXVSDKCDMSPPFPIEBTDOKGLQTIDIGSNEKEKLENSRLRSBDSPIKTS	490	SDIXVSDKCDMSPPFPIEBTDOKGLQTIDIGSNEKEKLENSRLRSBDSPIKTS	549	5.1	SDIXVSDKCDMSPPFPIEBTDOKGLQTIDIGSNEKEKLENSRLRSBDSPIKTS	490	
b	LSPTSKLQYSYSRDLDAKKGHLRSQTESPDADRTTNADHSSKVOHULSRQEL	603	603	LSPTSKLQYSYSRDLDAKKGHLRSQTESPDADRTTNADHSSKVOHULSRQEL	662	6.1	LSPTSKLQYSYSRDLDAKKGHLRSQTESPDADRTTNADHSSKVOHULSRQEL	603	LSPTSKLQYSYSRDLDAKKGHLRSQTESPDADRTTNADHSSKVOHULSRQEL	662	6.1	LSPTSKLQYSYSRDLDAKKGHLRSQTESPDADRTTNADHSSKVOHULSRQEL	603	
b	LSPTSKLQYSYSRDLDAKKGHLRSQTESPDADRTTNADHSSKVOHULSRQEL	550	550	LSPTSKLQYSYSRDLDAKKGHLRSQTESPDADRTTNADHSSKVOHULSRQEL	609	6.1	LSPTSKLQYSYSRDLDAKKGHLRSQTESPDADRTTNADHSSKVOHULSRQEL	550	LSPTSKLQYSYSRDLDAKKGHLRSQTESPDADRTTNADHSSKVOHULSRQEL	609	6.1	LSPTSKLQYSYSRDLDAKKGHLRSQTESPDADRTTNADHSSKVOHULSRQEL	550	
b	KERARVILQOARRDALAKKGANKINTTATPFCNRQLODEERRQRERARQLAAR	663	663	KERARVILQOARRDALAKKGANKINTTATPFCNRQLODEERRQRERARQLAAR	722	6.1	KERARVILQOARRDALAKKGANKINTTATPFCNRQLODEERRQRERARQLAAR	663	KERARVILQOARRDALAKKGANKINTTATPFCNRQLODEERRQRERARQLAAR	722	6.1	KERARVILQOARRDALAKKGANKINTTATPFCNRQLODEERRQRERARQLAAR	663	
b	KERARVILQOARRDALAKKGANKINTTATPFCNRQLODEERRQRERARQLAAR	610	610	KERARVILQOARRDALAKKGANKINTTATPFCNRQLODEERRQRERARQLAAR	669	6.1	KERARVILQOARRDALAKKGANKINTTATPFCNRQLODEERRQRERARQLAAR	610	KERARVILQOARRDALAKKGANKINTTATPFCNRQLODEERRQRERARQLAAR	669	6.1	KERARVILQOARRDALAKKGANKINTTATPFCNRQLODEERRQRERARQLAAR	610	
b	SGVNEBSPLSYGENAKKLKERAQKGENDNEDTTERIEPGVPGGGDNLNLNDL	723	7.2	SGVNEBSPLSYGENAKKLKERAQKGENDNEDTTERIEPGVPGGGDNLNLNDL	782	6.7	SGVNEBSPLSYGENAKKLKERAQKGENDNEDTTERIEPGVPGGGDNLNLNDL	723	SGVNEBSPLSYGENAKKLKERAQKGENDNEDTTERIEPGVPGGGDNLNLNDL	782	6.7	SGVNEBSPLSYGENAKKLKERAQKGENDNEDTTERIEPGVPGGGDNLNLNDL	723	
b	SGVNEBSPLSYGENAKKLKERAQKGENDNEDTTERIEPGVPGGGDNLNLNDL	670	670	SGVNEBSPLSYGENAKKLKERAQKGENDNEDTTERIEPGVPGGGDNLNLNDL	729	6.7	SGVNEBSPLSYGENAKKLKERAQKGENDNEDTTERIEPGVPGGGDNLNLNDL	670	SGVNEBSPLSYGENAKKLKERAQKGENDNEDTTERIEPGVPGGGDNLNLNDL	729	6.7	SGVNEBSPLSYGENAKKLKERAQKGENDNEDTTERIEPGVPGGGDNLNLNDL	670	
b	DTPQNSKLVLKLUKJLEVQVANSSAQAQKAVTTESSBQDMKSGTBDRTERLOKTT	783	7.8	DTPQNSKLVLKLUKJLEVQVANSSAQAQKAVTTESSBQDMKSGTBDRTERLOKTT	842	7.3	DTPQNSKLVLKLUKJLEVQVANSSAQAQKAVTTESSBQDMKSGTBDRTERLOKTT	783	DTPQNSKLVLKLUKJLEVQVANSSAQAQKAVTTESSBQDMKSGTBDRTERLOKTT	842	7.3	DTPQNSKLVLKLUKJLEVQVANSSAQAQKAVTTESSBQDMKSGTBDRTERLOKTT	783	
b	DTPQNSKLVLKLUKJLEVQVANSSAQAQKAVTTESSBQDMKSGTBDRTERLOKTT	730	7.3	DTPQNSKLVLKLUKJLEVQVANSSAQAQKAVTTESSBQDMKSGTBDRTERLOKTT	789	7.3	DTPQNSKLVLKLUKJLEVQVANSSAQAQKAVTTESSBQDMKSGTBDRTERLOKTT	730	DTPQNSKLVLKLUKJLEVQVANSSAQAQKAVTTESSBQDMKSGTBDRTERLOKTT	789	7.3	DTPQNSKLVLKLUKJLEVQVANSSAQAQKAVTTESSBQDMKSGTBDRTERLOKTT	730	
b	SEBVTNLKGPKDOSYQVGLAALENEKQDTRAVERKRYLMGTRNTERBAMQ	843	8.4	SEBVTNLKGPKDOSYQVGLAALENEKQDTRAVERKRYLMGTRNTERBAMQ	902	8.4	SEBVTNLKGPKDOSYQVGLAALENEKQDTRAVERKRYLMGTRNTERBAMQ	843	SEBVTNLKGPKDOSYQVGLAALENEKQDTRAVERKRYLMGTRNTERBAMQ	902	8.4	SEBVTNLKGPKDOSYQVGLAALENEKQDTRAVERKRYLMGTRNTERBAMQ	843	
b	SEBVTNLKGPKDOSYQVGLAALENEKQDTRAVERKRYLMGTRNTERBAMQ	850	8.5	SEBVTNLKGPKDOSYQVGLAALENEKQDTRAVERKRYLMGTRNTERBAMQ	909	8.5	SEBVTNLKGPKDOSYQVGLAALENEKQDTRAVERKRYLMGTRNTERBAMQ	850	SEBVTNLKGPKDOSYQVGLAALENEKQDTRAVERKRYLMGTRNTERBAMQ	909	8.5	SEBVTNLKGPKDOSYQVGLAALENEKQDTRAVERKRYLMGTRNTERBAMQ	850	
b	ERFRNPVPUFSKDRTRKQLOFSQYINRPEMKRQSIQEDTKGNEKAITEORKP	790	7.9	ERFRNPVPUFSKDRTRKQLOFSQYINRPEMKRQSIQEDTKGNEKAITEORKP	849	7.9	ERFRNPVPUFSKDRTRKQLOFSQYINRPEMKRQSIQEDTKGNEKAITEORKP	790	ERFRNPVPUFSKDRTRKQLOFSQYINRPEMKRQSIQEDTKGNEKAITEORKP	849	7.9	ERFRNPVPUFSKDRTRKQLOFSQYINRPEMKRQSIQEDTKGNEKAITEORKP	790	
b	EWMLVNUKGQALLRMNOISLJEKHDLERRYSLNRLRAMIAEDWQKTAQKREL	953	9.5	EWMLVNUKGQALLRMNOISLJEKHDLERRYSLNRLRAMIAEDWQKTAQKREL	1022	9.5	EWMLVNUKGQALLRMNOISLJEKHDLERRYSLNRLRAMIAEDWQKTAQKREL	953	EWMLVNUKGQALLRMNOISLJEKHDLERRYSLNRLRAMIAEDWQKTAQKREL	1022	9.5	EWMLVNUKGQALLRMNOISLJEKHDLERRYSLNRLRAMIAEDWQKTAQKREL	953	

XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Weirman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX DR WPI; 2001-442233/47.  
DR N-P5B; AAI60264.

XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.

XX  
Example 2, SEQ ID NO 6039; 10078PP; English.

XX  
CC The invention relates to human nucleic acids (AA157798-AAI61369) and the  
CC encoded polypeptides (AA138643-AAW42213) with nootropic,  
CC immunosuppressant and cytoprotective activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Sly-Drager Syndrome. Other uses include the  
utilisation of the activities such as: Immune system suppression, haemostatic  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patient did not form  
CC part of the printed specification

SQ Sequence 1023 AA;

XX

Query Match	93.9%; Score 5152; DB 4; Length 1023;
Best local Similarity	99.3%; Pred. No. 3..1e-309;
Matches	1007; Conservative 3; Mismatches 4;
QY	63 IGNLJDPERDNEEDDENRVRNQEERAKAKITELINKLNFLRAKOLATVNPNPDDPDRAR 122
Db	10 LANJJDDEEFDNEDDENRVRNQEERAKAKITELINKLNFLRAKOLATVNPNPDDPDRAR 122
QY	123 LNPFGDPDSEEPETASPRKTESFYNNSYNPKEVTPQYLNPPDEPAFTVKDSP 182
Db	70 LNPFGDPDSEEPETASPRKTESFYNNSYNPKEVTPQYLNPPDEPAFTVKDSP 182
QY	183 OSTKRKNIRPVDMSKLYADSKTEBEELDESBNPPYEPKSTPPRNVLVPQLETERV 242
Db	130 OSTKRKNIRPVDMSKLYADSKTEBEELDESBNPPYEPKSTPPRNVLVPQLETERV 189
QY	243 KRKAAPPVILSKPGTGVNLNTVSAGCKLDTSPKSPKSPIRPUVLSRKPKRNQASLLWCKEVT 302
Db	190 KRKAAPPVILSKPGTGVNLNTVSAGCKLDTSPKSPKSPIRPUVLSRKPKRNQASLLWCKEVT 249
QY	303 KNYKGKVNFTTSRNGLSPCAALHFRPDLLIYKSLAQDICKENKKGAYGEGASIGS 362
Db	250 KNYKGKVNFTTSRNGLSPCAALHFRPDLLIYKSLAQDICKENKKGAYGEGASIGS 369
QY	363 RLLRPSDMVLLAIKDPLTWTMILQIARHFSQBLANVOIBENSSTKVGNVETDMS 422
Db	310 RLLRPSDMVLLAIKDPLTWTMILQIARHFSQBLANVOIBENSSTKVGNVETDMS 369
QY	423 SVDOBKFYABLSDLKREPELQOPIGAVPLSQQDSVFTNDSGYGESEBHTQFDDHSP 482
Db	370 SVDOBKFYABLSDLKREPELQOPIGAVPLSQQDSVFTNDSGYGESEBHTQFDDHSP 429
QY	483 STASPYCRAFTSKDTEPOKSQQSSRTSGDGGCSNTSTQAQVLAGKRLIAKETRL 542
Db	430 STASPYCRAFTSKDTEPOKSQQSSRTSGDGGCSNTSTQAQVLAGKRLIAKETRL 489
QY	543 SLYVSDKKDMSPFICETDEQKLQTIDGSNLKEKLNRSLECRSPESPIKTS 602
Db	490 SLYVSDKKDMSPFICETDEQKLQTIDGSNLKEKLNRSLECRSPESPIKTS 549
QY	603 LSPTSKLGYSYSDLDLAKKKHASLRQTESSDPADRTTLNHAHDSSKTVORHLISROBL 662
Db	550 LSPTSKLGYSYSDLDLAKKKHASLRQTESSDPADRTTLNHAHDSSKTVORHLISROBL 609
QY	663 KERARVLLQARRDALKAGKHNHTNTAPCPNRLDQDDEERRQLRERARLIAEAR 722
Db	610 KERARVLLQARRDALKAGKHNHTNTAPCPNRLDQDDEERRQLRERARLIAEAR 669
QY	723 SGVKMSELPSSYEMARKURKERSKASGDENDNIEDTNEIEPEGFWVGGADELTNLEND 782
Db	670 SGGMSELPSSYGERBAKURKERSKASGDENDNIEDTNEIEPEGFWVGGADELTNLEND 729
QY	783 DTPEQNSKLVDLKKLLEVOPOVANSPPSAQAKAVTSESEQDKMSGTRDLTERLQKTT 842
Db	730 DTPEQNSKLVDLKKLLEVOPOVANSPPSAQAKAVTSESEQDKMSGTRDLTERLQKTT 789
QY	843 ERFPNPPVYESKDSWTRKTOLOGSQYIERNPEMRSIQEDTKRGNSRKAATETOKP 902
Db	790 ERFPNPPVYESKDSWTRKTOLOGSQYIERNPEMRSIQEDTKRGNSRKAATETOKP 849
QY	903 SEDEVLNKGPKDSQYVGRMLAENEOKDTRAALVEKRLIMDFGRNTBREAMQ 962
Db	850 SEDEVLNKGPKDSQYVGRMLAENEOKDTRAALVEKRLIMDFGRNTBREAMQ 909
QY	963 EWFMLVNLKGNALLRRMNQSLILEGEHDLLERYELLNRERLRAMLAEDWORTAQKRRQL 1022
Db	910 EWFMLVNLKGNALLRRMNQSLILEGEHDLLERYELLNRERLRAMLAEDWORTAQKRRQL 969
QY	1023 LDELVALVNLKRNDAVLVRDIDAQEQAEEDHEBERTLSQNGKMKAKBCKVHQ 1076
Db	970 LDELVALVNLKRNDAVLVRDIDAQEQAEEDHEBERTLSQNGKMKAKBCKVHQ 1023

RESULT 10  
 ARB1081  
 ID ARB1081 standard; protein; 1023 AA.  
 XX  
 AC ARB1081;  
 XX  
 DE Novel human polypeptide SEQ ID NO 1775.  
 XX  
 KW vulnerability; CNS-gen.; gene therapy; diagnostic; forensic; mapping;  
 DNA purification; protein purification; osteoarthritis; antiarthritic;  
 osteopathic; musculoskeletal disease; osteoporosis; endocrine disease;  
 periodontal disease; antiinflammatory; mouth disease; burns; injury;  
 peripheral neuropathy; Alzheimers disease; neuroprotective; nortropic;  
 degeneration; parkinsons disease; antiparkinsonian; neurological disease;  
 cerebrovascular ischemia; cerebroprotective; vasotrophic;  
 cardiovascular disease; autoimmune disease; immunosuppressive;  
 immune disorder; viral infection; virucide; infection; cancer;  
 cytostatic; neoplasm.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005049806-A2.  
 XX  
 PD 02-JUN-2005.  
 XX  
 PR 11-MAR-2004; 2004WO-US007412.  
 XX  
 PR 14-MAR-2003; 2003US-00389559.  
 XX  
 PA (NUTIVE-) NUVELLO INC.  
 XX  
 PI Tang T<sup>Y</sup>, Wang J, Zhang J, Ren F, Zhou P, Ma Y, Chen R;  
 PI Ghosh M, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R;  
 PI Wehrman T, Weng G, Boyle B;  
 XX  
 DR WPI: 2005-4117730/42.

New Polynucleotide encoding a polypeptide with biological activity, useful for treating a disease or disorder, e.g. osteoarthritis, burns, CNS and peripheral disease, stroke, autoimmune disorders, viral infection, or cancer.

Example 3: SEQ ID NO 1775; 500pp; English.

CC The invention describes a new isolated polynucleotide comprising: a nucleotide sequence of polypeptide with biological activity comprising: a nucleotide sequence that hybridizes to the sequence of (i) under stringent hybridization conditions; or a nucleotide sequence having greater than 99% sequence identity with the sequence of (i). Also described are: a(n) (expression)vector comprising (i); a host cell genetically engineered to comprise (i) operatively, associated with a regulatory sequence that modulates expression of the polypeptide in the host cell; an isolated polypeptide comprising a polynucleotide in the host cell; an isolated polypeptide comprising a sequence of SEQ ID NOS: 560-1134 (fully defined), where the polypeptide is: a polypeptide encoded by (i); or a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NOS: 1-567; a composition comprising the polypeptide of (i) and a carrier; an antibody directed against the polypeptide of (i); a method for detecting (i) in a sample; a method for detecting the polypeptide of (i) in a sample; a method for identifying a compound that binds to the polypeptide of (i); a method of producing the polypeptide of (i); and a collection of polynucleotides, where the collection comprising of at least one of SEQ ID NOS: 1-567. (i) is a polynucleotide comprising any of the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological activity, which comprises any of the amino acid sequence of SEQ ID NOS: 568-1134. All sequences are fully defined in the specification. The sequences and methods are useful in diagnostics, forensic, and gene mapping, in identifying of mutations responsible for genetic disorders or other traits, in assessing biodiversity, and for producing many other types of data and products dependent on DNA and amino acid sequences. The

composition and method are useful for treating a disease or disorder, e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and peripheral disease, Alzheimer's disease, Parkinson's disease, stroke, autoimmune disorders, viral infection, or cancer. This is the amino acid sequence of a novel polypeptide of the invention.

SQ Sequence 1023 AA;

Query Match 93.9%; Score 5152; DB 9; Length 1023;  
Best Local Similarity 99.3%; Pred. No. 3.1e-309;  
Matches 1007; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 63 IGNLDPEEEDTDDENRVMQEKAKITEINKUNPLDEBKDLATVNSNPPDPAE  
; : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 10 LANLDDPFBEDNEBDDENRVMQEKAKITEINKUNPLDEBKDLATVNSNPPDPAE 69  
Qy 123 LNPFGDPDSSEPRITETASPRKTEDSFNNSYNPKEVQTEQYLNIPDEPERAVTIKDSP 182  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 70 LNPGDGPDSSEPRITETASPRKTEDSFNNSYNPKEVQTEQYLNIPDEPERAVTIKDSP 129  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Qy 183 OSTKRKNIRPVDMSKYLADSSKTERELBDSBNPFPYKSTPPPNLUNPVQELEBERRY 242  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 130 OSTKRKNIRPVDMSKYLADSSKTERELBDSBNPFPYKSTPPPNLUNPVQELEBERRY 189  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Qy 243 KRKAAPPVPLSPKGTVLAVNTVSACKLSTSRSKPSIPSPVGLGRPKNAQSLLWCKET 302  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 190 KRKAAPPVPLSPKGTVLAVNTVSACKLSTSRSKPSIPSPVGLGRPKNAQSLLWCKET 249  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Qy 303 KNYRGKIKNTFTSWSRNGLSSCALLAHFRPDLDIYKLNDQDIKENNKAGDGASIGIS 362  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 250 KNYRGKIKNTFTSWSRNGLSSCALLAHFRPDLDIYKLNDQDIKENNKAGDGASIGIS 309  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Qy 363 RLLERPSDMVLAIAIPDKLTWVYKQRAHSGQBLNVOIEENSSKTYKGNTEDTNS 422  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 310 RLLERPSDMVLAIAIPDKLTWVYKQRAHSGQBLNVOIEENSSKTYKGNTEDTNS 369  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Qy 423 SVDQEKPYAISLSLDRKREPELQPTGSAVDPISQDPSVFDGCGESSEHQTDPHSLP 482  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 370 SVDQEKPYAISLSLDRKREPELQPTGSAVDPISQDPSVFDGCGESSEHQTDPHSLP 429  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Qy 483 STASYCRRKSDTPOKSQSGRTSGSDPGICNTSITQAQLIGKERRLKARTEL 542  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 430 STASYCRRKSDTPOKSQSGRTSGSDPGICNTSITQAQLIGKERRLKARTEL 489  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Qy 543 SDLYVSDKKKDMSPPFICEBTDRQKLQTLDGSNLREKLNRSLSBCKSDPESPIKTS 602  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 490 SDLYVSDKKKDMSPPFICEBTDRQKLQTLDGSNLREKLNRSLSBCKSDPESPIKTS 549  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Qy 603 LSPTSKLGYSYSDLDLAKCHASHLQRQTSDDPDRDTTNAHADISSKTVORHLRSQEL 662  
550 LSPTSKLGYSYSDLDLAKCHASHLQRQTSDDPDRDTTNAHADISSKTVORHLRSQEL 609  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 663 KERARVILLEGARRDAALKAGKHNNTATPFCNRQSLDQODBERRQLRERRAOLIAEAR 722  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Qy 610 KERARVILLEGARRDAALKAGKHNNTAFCNRQSLDQODBERRQLRERRAOLIAEAR 669  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 723 SGVKMSBELPSYGEMAAKLUERSKASGDEDNDTRDNTSEPIEGFWGAGDBLTLENDL 782  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 670 SGVKMSBELPSYGEMAAKLUERSKASGDEDNDTRDNTSEPIEGFWGAGDBLTLENDL 729  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Qy 783 DTPBONSKLVLKLUCKLKVOPQVANSPPSAQAKVTESEBQDMKSGTDLRTERLOKT 842  
730 DTPBONSKLVLKLUCKLKVOPQVANSPPSAQAKVTESEBQDMKSGTDLRTERLOKT 789  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 843 BRFRNPVVKSDTRKTOQFSQYIENPEMKRQSISQBDTKKGNEKAALTETOKP 902  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 790 ERFRNPVVKSDTRKTOQFSQYIENPEMKRQSISQBDTKKGNEKAALTETOKP 849  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Qy 903 SEDDEVLINKGKFDTTSOYVGRLALALENEQKOIDTRALVEKLRVIMDTERNTERBAMO 962  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db 850 SEDDEVLINKGKFDSQQVVGRLALALENBOKIDTRALVEKLRVIMDTERNTERBAMO 909  
| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Qy 963 EWFMLVNUKQKALIRRNQQLSLEKEHDLERYELLNRBLRMLATEDWQKTEAQKREGQI 1022

RESULT 11  
DB 910 EWFMLVNUKQKALIRRNQQLSLEKEHDLERYELLNRBLRMLATEDWQKTEAQKREGQI 969  
ID AEA21082 standard; protein; 1023 AA.  
AC AEA21082;  
XX DT 11-AUG-2005 (first entry)  
DE Novel human polypeptide SEQ ID NO 1776.  
KW vulnary; CNS-gen.; gene therapy; diagnostic; forensic; mapping;  
KW DNA purification; protein purification; osteoarthritis;  
KW osteoporotic; musculoskeletal disease; endocrine disease;  
KW periodontal disease; antiinflammatory; mouth disease; burns; injury;  
KW peripheral neuropathy; Alzheimer's disease; neuroprotective; nontropic;  
KW degeneration; parkinsons disease; antiparkinsonian; neurological disease;  
KW cerebrovascular ischemia; cerebroprotective; vasotrophic;  
KW cardiovascular disease; autoimmune disease; immunosuppressive;  
immune disorder; viral infection; virucide; infection; cancer;  
KW cytostatic; neoplasm.  
XX OS Homo sapiens.  
XX PN WO2005049806-A2.  
XX PR 14-MAR-2003; 2003US-00389559.  
XX PD 02-JUN-2005.  
XX PA (NUVO) NUVOLO INC.  
XX PI Tang YY, Wang J, Zhang J, Ren F, Zhou P, Ma Y;  
PI Ghosh M, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R;  
PI Weinman T, Weng G, Boyle B;  
XX DR WPI; 2005-41773042.  
XX PS New polynucleotide encoding a polypeptide with biological activity, useful for treating a disease or disorder, e.g. osteoarthritis, burns, CNS and peripheral disease, stroke, autoimmune disorders, viral infection, or cancer.  
XX Example 3; SEQ ID NO 1776; 500PP; English.  
CC The invention describes a new isolated polynucleotide (1) encoding a polypeptide with biological activity comprising: a nucleotide sequence of SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes to the sequence of (1) under stringent hybridization conditions; or a nucleotide sequence having greater than 95% sequence identity with the sequence of (1). Also described are: a(n) (expression) vector comprising (1), a host cell genetically engineered to comprise (1) operatively, associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell; an isolated polypeptide comprising a sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide is: a polypeptide encoded by (1); or a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NOS: 1-567; a composition comprising the polypeptide of (3) and a carrier; an antibody directed against the polypeptide of (3); a method for detecting (1) in a sample; a method for detecting the polypeptide of (3) in a sample; a method for identifying a compound that binds to the polypeptide of (3); a method of producing the polypeptide of (3); and a collection of polynucleotides, where the collection comprising of at least one of SEQ ID NOS: 1-567. (1) is a polynucleotide comprising any of

Page 12

CC the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological activity, which comprises any of the amino acid sequence of SEQ ID NOS: 568-1134. All sequences are fully defined in the specification. The CC sequences and methods are useful in diagnostics, forensic, and gene CC mapping, in identifying of mutations responsible for genetic disorders or CC other traits, in assessing biodiversity, and for producing many other CC types of data and products dependent on DNA and amino acid sequences. The CC composition and method are useful for treating a disease or disorder, e.g., osteoporosis, osteoarthritis, periodontal disease, burns, CNS and CC peripheral disease, Alzheimer's disease, Parkinson's disease, stroke, CC autoimmune disorders, viral infection, or cancer. This is the amino acid CC sequence of a novel polypeptide of the invention.

XX

SQ Sequence 1023 AA;

Db	790	ERFRNPVVFPSKOSTVRKTQLOFSQYIENRPEMKRQSIOBTKKGNEKEAITEQRKP	849
Qy	903	SEBVLNKGPKOTSQYNGELALENSQKQDITRAALVEKURLYMDTGRNTERBBAMMQ	962
Db	850	SEBVLNKGPKOSQYVGELALENSQKQDITRAALVEKURLYMDTGRNTERBBAMMQ	909
Qy	963	EWMLNLVKNNALTTRMANOLSLIEKEHDLBRYELLURBLRAMLAIEDWQKTEAQKBROL	1022
Db	910	EWMLNLVKNNALTTRMANOLSLIEKEHDLBRYELLURBLRAMLAIEDWQKTEAQKBROL	969
Qy	1023	LUDBLVALVNKRDALVLDLDAQKAFREDEDELERLTQKNGKGMKKEKCVLQ	1076
Db	970	LUDBLVALVNKRDALVLDLDAQKAFREDEDELERLTQKNGKGMKKEKCVLQ	1023

CC polynucleotide hybridizing under stringent conditions with any one of SEQ ID NOS: 1-567; a composition comprising the polypeptide of (3); and a polypeptide of (1) in sample; a method for detecting the polypeptide of (3); a method for detecting (1) in sample; a method for identifying a compound that binds to the collection of polynucleotides, where the collection comprising of at least one of SEQ ID NOS: 1-567. (1) is a polynucleotide comprising any of the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological activity, which comprises any of the amino acid sequence of SEQ ID NOS: 568-1134. All sequences are fully defined in the specification. The sequences and methods are useful in diagnostics, forensic, and gene mapping, in identifying mutations responsible for genetic disorders or other traits, in assessing biodiversity, and for producing many other types of data and products dependent on DNA and amino acid sequences. The composition and method are useful for treating a disease or disorder, e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and peripheral disease, Alzheimer's disease, Parkinson's disease, stroke, autoimmune disorders, viral infection, or cancer. This is the amino acid sequence of a novel polypeptide of the invention.

SQ Sequence 996 AA;

Query Match Best Local Similarity 99.4%; Score 5037; DB 9; Length 996; Matches 986; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 85 EKAAKUTELINKUNFLDEAEDLATINSNPDPDAELAMPGRDPESEPTETASPRK 144

Db 5 KSAASBEELBLKLNFIDAEEDLATINSNPDPDAELAMPGRDPESEPTETASPRK 64

QY 145 EDSFTINNSYNPKVEQVTPQINAPPDEAFTIKOSPPOSTKRKNTRPVDMSKYIADSS 204

Db 65 EDSFTINNSYNPKVEQVTPQINAPPDEAFTIKOSPPOSTKRKNTRPVDMSKYIADSS 124

QY 205 KTEEBEELDESNPFYERKSTPPPNLYNPVQDELETERVRKAPAPPLSPRTGIVAMENTV 264

Db 125 KTEEBEELDESNPFYERKSTPPPNLYNPVQDELETERVRKAPAPPLSPRTGIVAMENTV 184

QY 265 SAGKDLSTSPPSPSPPSPVGRKPNASOILWMCCKTUVKGRVKUTNFTTSWRNGLSC 324

Db 185 SAGKDLSTSPPSPSPPSPVGRKPNASOILWMCCKTUVKGRVKUTNFTTSWRNGLSC 244

QY 325 ALHHRFPDLIDYKSLANPODKKENNKAYDGPASIGISRLKPSDMLVLAIPDKLTVTY 384

Db 245 ALHHRFPDLIDYKSLANPODKKENNKAYDGPASIGISRLKPSDMLVLAIPDKLTVTY 304

QY 385 LYQIRAHFSGBLNVYQIBERNISKSYKVENYETITNSVYDQEKTYAELSDKRBPELOO 444

Db 305 LYQIRAHFSGBLNVYQIBERNISKSYKVENYETITNSVYDQEKTYAELSDKRBPELOO 364

QY 445 PISGAVDPLSODDSYEVNGVGEBEBSEHOTPDHLSPSSTASPCKRTSDTERQKSQS 504

Db 365 PISGAVDPLSODDSYEVNGVGEBEBSEHOTPDHLSPSSTASPCKRTSDTERQKSQS 424

QY 505 SGRTSGSDDPGEICSNSTDQJQVNLGKKRKAETELSLDLYVSDKKMSPPFCEBD 564

Db 425 SGRTSGSDDPGEICSNSTDQJQVNLGKKRKAETELSLDLYVSDKKMSPPFCEBD 484

QY 565 EOKLQTDIGSNELEKKEKLNSRLCRSDPSPKTKTSLSPTSKLGYSYRDLAKKH 624

Db 485 EOKLQTDIGSNELEKKEKLNSRLCRSDPSPKTKTSLSPTSKLGYSYRDLAKKH 544

QY 625 ASLROTESPDADRTTINHADHSSKLVORHULSROELKERARRVULQARDRAALKAGNK 684

Db 545 ASLROTESPDADRTTINHADHSSKLVORHULSROELKERARRVULQARDRAALKAGNK 604

QY 685 HNTNTATPPCRQLSQQDERRQERARQLIARSGKMSLPSKEMAEKLER 744

Db 605 HNTNTATPPCRQLSQQDERRQERARQLIARSGKMSLPSKEMAEKLER 664

QY 745 SKASGDENDNTEIDTNERBIEGFVWGGDELTNLENDDTPEQNSKVLVDJKLKKLLEVQP 804

RESULT 13

AAM39322

ID AAM39322 standard; protein; 996 AA.

XX

AC AAM39322;

XX

DT 22-OCT-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 2467.

XX

Human; notropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemoractic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.

XX

KW

OS Homo sapiens.

XX

PN WO200153312-A1.

XX

PD 26-JUL-2001.

XX

PP 26-DEC-2000; 2000WO-US034263.

XX

PR 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-0052317.

PR 20-JUN-2000; 2000US-0059842.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-0053450.

PR 14-SEP-2000; 2000US-0062191.

PR 19-OCT-2000; 2000US-00633036.

PR 29-NOV-2000; 2000US-00727344.

XX

(HYSEQ HYSEQ INC.

XX

Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

PI Zhou P, Goodrich R, Drmanac RT;

XX

DR WPI; 2001-442253/47.

DR N-PDB; AAI58478.

XX

Novel nucleic acids and polypeptides, useful for treating disorders such

as central nervous system injuries.

XX

Example 4; SEQ ID NO 2467; 1078pp; English.

XX

The invention relates to human nucleic acids (AAI57798-AAI61369) and the

CC encoded polypeptides (AM38642-AM42213) with nootropic, CC immunosuppressant and cytostatic activity. The polynucleotides are useful CC in gene therapy. A composition containing a polypeptide or polynucleotide CC of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and CC localised neuropathies and central nervous system diseases, such as CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC utilisation of the activities such as: immune system suppression, CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic CC and thrombolytic activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukemias and CC C.N.S disorders. Note: The sequence data for this patent did not form CC part of the printed specification.

xx

SQ Sequence 996 AA;

Query Match Best Local Similarity 99.3%; Pred. No. 6.7e-302; Length 996; Matches 985; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 85 EKAAKITELINKUNLDEAKKIAATUNSPFDAAEINPFGPDPSEPIERASPKT 144

Db : ; 5 KSAASSEELINKUNLDEAKKIAATUNSPFDAAEINPFGPDPSEPIERASPKT 64

QY 145 DSDPNSTNVPKEVQTPQNLPEDEPEARTIKDOSPPOSTKRNIRPVDMKLYADSS 204

Db 65 BDFNINSTNPVKEVQTPQNLPEDEPEARTIKDOSPPOSTKRNIRPVDMKLYADSS 124

QY 205 KTEFELDLSNPFPYEPKSTPPPNLVLNPYQEBELETERVVKRKAAPVPSPKTGLENNTY 264

Db 125 KTEFELDLSNPFPYEPKSTPPPNLVLNPYQEBELETERVVKRKAAPVPSPKTGLENNTY 184

QY 265 SAGKLSTSPKSPSIPSPVPLGKRNENASQSLWKEVTKYNGKLTNPWSRNGLFC 324

Db 185 SAGKLSTSPKSPSIPSPVPLGKRNENASQSLWKEVTKYNGKLTNPWSRNGLFC 244

QY 325 ALIHFHRPDIDYKSLNPDQDKKENKKAYDGASIGSRLLEPSDMVLAIPDKLTVTY 384

Db 245 ALIHFHRPDIDYKSLNPDQDKKENKKAYDGASIGSRLLEPSDMVLAIPDKLTVTY 384

QY 385 LYQIRAHFSQEQLNVYQIEBNNSKSYKVGMYETDTNSVDQKRYAELSLDKREPELQQ 444

Db 305 LYQIRAHFSQEQLNVYQIEBNNSKSYKVGMYETDTNSVDQKRYAELSLDKREPELQQ 364

QY 445 PISGAVIDFISODDSVYEVNDGGGSESENHOTPDHLSPSTASPVCRTYSDTRQKQOS 504

Db 365 PISGAVIDFISODDSVYEVNDGGGSESENHOTPDHLSPSTASPVCRTYSDTRQKQOS 424

QY 505 SGRTSGSDPGICNTSDAQVQLGKKLKAETLESLDLYSDKKDKMSPPPICEED 564

Db 425 SGRTSGSDPGICNTSDAQVQLGKKLKAETLESLDLYSDKKDKMSPPPICEED 484

QY 565 EOKLQTLDTGSNLERKEKLNRSLCSDPESPKTTSISPTSKLGYSYSRDLAKKKH 624

Db 485 EOKLQTLDTGSNLERKEKLNRSLCSDPESPKTTSISPTSKLGYSYSRDLAKKKH 544

QY 625 ASURQTESUPPADRTLNHADHSKIVORLSLQELKERRARVILEBRDALKAGNK 684

Db 545 ASURQTESUPPADRTLNHADHSKIVORLSLQELKERRARVILEBRDALKAGNK 604

QY 685 HNTNTATPPCNRQLSDQDERRRQLRERARQLIARSGVMSLPSYGERMAEKLER 144

Db 605 HNTNTATPPCNRQLSDQDERRRQLRERARQLIARSGVMSLPSYGERMAEKLER 664

QY 745 SKASGDEDNNIEEIDNEEIPGFVNGGGDELNLENDLDTPEONQSKLVDLKKLLEQWP 804

Db 665 SKASGDEDNNIEEIDNEEIPGFVNGGGDELNLENDLDTPEONQSKLVDLKKLLEQWP 724

QY 805 QVANSPSSAQAKVTESSQDMKGSTEDRTERQKTERPRPWRVPSDSTRKTOQS 864

Db 725 QVANSPSSAQAKVTESSQDMKGSTEDRTERQKTERPRPWRVPSDSTRKTOQS 784

QY 865 PSQYIENRPEMKRSIQBDTGGKNEGEKAITSTORKSBSDEVLANKGKTSQVVGSLA 924

Db 785 FSQYIENRPEMKRSIQBDTGGKNEGEKAITSTORKSBSDEVLANKGKTSQVVGSLA 844

QY 925 ALENEQKQDTRAALVERKLYMDTGNTTEBAMMWFVNKGALIRMNQSL 984

Db 845 ALENEQKQDTRAALVERKLYMDTGNTTEBAMMWFVNKGALIRMNQSL 904

QY 985 BKEDBLERYELLNLRELKMLATEDWOTCAOKRREGOLLDDELVALVNRDALVRDJAQ 1044

Db 905 BKEDBLERYELLNLRELKMLATEDWOTCAOKRREGOLLDDELVALVNRDALVRDJAQ 964

QY 1045 EKQAREEBEHLTLEQNQGKMAKKECVLQ 1076

Db 965 EKQAREEBEHLTLEQNQGKMAKKECVLQ 996

RESULT 14

AER2069 ID AER2069 Standard; protein; 960 AA.

XX

AC AER2069:

XX

DT 11-AUG-2005 (first entry)

XX

DE Novel human polypeptide SEQ ID NO 963.

XX

KW vulnary; CNS-gen.; gene therapy; diagnostic; forensic; mapping;

XX

KW DNA purification; protein purification; osteoarthritis; antiarthritic;

XX

KW osteoparification; musculoskeletal disease; endocrine disease;

XX

KW periodontal disease; antiinflammatory; mouth disease; burns; injury;

XX

KW peripheral neuropathy; Alzheimer's disease; neuroprotective; nontropic;

XX

KW degeneration; Parkinson's disease; antiparkinsonian; neurological disease;

XX

KW cerebrovascular; ischemia; cerebroprotective; vasotropic;

XX

KW cardiovascular disease; autoimmune disease; immunosuppressive;

XX

KW cytotstatic; viral infection; vincicide; infection; cancer;

XX

OS Homo sapiens.

XX

PN WO200549806-A2.

XX

PD 02-JUN-2005.

XX

PP 11-MAR-2004; 2004WO-US007412.

XX

PR 14-MAR-2003; 2003US-00389559.

XX

PA (NUVE-) NUVELO INC.

XX

Tang TY, Wang J, Zhang J, Ren F, Zhou P, Ma Y,

PT Ghosh M, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R;

PT Wehrman T, Weng G, Boyle B;

XX

DR WPI; 2005-4173042.

XX

N-PSDB; AEA19702.

XX

PT New polynucleotide encoding a polypeptide with biological activity,

PT useful for treating a disease or disorder, e.g. osteoarthritis, burns,

PT CNS and peripheral disease, stroke, autoimmune disorders, viral

PT infection, or cancer.

XX

Claim 20; SEQ ID NO 963; 500pp; English.

XX

The invention describes a new isolated polynucleotide (I) encoding a

CC polypeptide with biological activity comprising: a nucleotide sequence of

CC SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes

CC to the sequence of (1) under stringent hybridization conditions; or a

CC nucleotide sequence having greater than 99% sequence identity with the

CC sequence of (1). Also described are: (a(n)) (expression)vector comprising

(1); a host cell genetically engineered to comprise (1) operatively,

CC associated with a regulatory sequence that modulates expression of the

polynucleotide in the host cell; an isolated polypeptide comprising a

CC sequence of SEQ ID NOS: 569-1134 (fully defined), where the polypeptide  
 CC is: a polypeptide encoded by (1); or a polypeptide encoded by a  
 CC polynucleotide hybridizing under stringent conditions with any one of SEQ  
 CC ID NOS: 1-567; a composition comprising the polypeptide of (3) and a  
 carrier; an antibody directed against the polypeptide of (3); a method  
 for detecting (1) in a sample; a method for detecting the polypeptide of  
 (3) in a sample; a method for identifying a compound that binds to the  
 polypeptide of (3); a method of producing the polypeptide of (3); and a  
 collection of polynucleotides, where the collection comprising of at  
 least one of SEQ ID NOS: 1-567. (1) is a polynucleotide comprising any of  
 the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological  
 activity, which comprises any of the amino acid sequence of SEQ ID NOS:  
 CC 568-1134. All sequences are fully defined in the specification. The  
 CC sequences and methods are useful in diagnostics, forensic, and gene  
 CC mapping, in identifying mutations, for genetic disorders or  
 other traits, in assessing biodiversity, and for producing many other  
 types of data and products dependent on DNA and amino acid sequences. The  
 CC composition and method are useful for treating a disease or disorder,  
 e.g., osteoporosis, osteoarthritis, periodontal disease, burns, CNS and  
 CC peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,  
 CC autoimmune disorders, viral infection, or cancer. This is the amino acid  
 CC sequence of a novel polypeptide of the invention.

SQ Sequence 960 AA:

Query Match 87.8%; Score 4817; DB 9; Length 960;

Best Local Similarity 95.8%; Pred. No. 1; 4e-288; Matches 950; Conservative 2; Mismatches 4; Indels 36; Gaps 1; Qy 85 EKAKAKITELINKLNFLDEBKBDAEKLATVNNSPPDPDAEKLNPFGDPSERPI-TETASPRK 144 Db 5 RSASSSBELLINKLNFLDEBKBDAEKLATVNNSPPDPDAEKLNPFGDPSERPI-TETASPRK 64 Qy 145 EDSFVNVNSYNNPKEVQTPQXINPDPERARTIKOSPPQSTKRKRIPVDMISKYADSS 204 Db 65 EDSFVNVNSYNNPKEVQTPQXINPDPERARTIKOSPPQSTKRKRIPVDMISKYADSS 124 Qy 205 KTEEBEELDESMPFPYERKSTPPPNLNVPEBELETERVKRKAAPPVPLSPKGIVAMENTV 264 Db 125 KTEEBEELDESMPFPYERKSTPPPNLNVPEBELETERVKRKAAPPVPLSPKGIVAMENTV 184 Qy 265 SAGKOLSLSTSPPSPSPTSPVPLGKPKNPAQSLLNWCKEVTKYRGKVNFTPSWRNGLSFC 324 Db 185 SAGKOLSLSTSPPSPSPTSPVPLGKPKNPAQSLLNWCKEVTKYRGKVNFTPSWRNGLSFC 244 Qy 325 ALIHLHRPDULDYKSLNPQDKKENKAYDQFASIGISRLPEPSDMLLAPDKLTUMTY 384 Db 245 ALIHLHRPDULDYKSLNPQDKKENKAYDQFASIGISRLPEPSDMLLAPDKLTUMTY 304 Qy 385 IYQIRAHFSGOELNVVQIEENNSKSTYKVGMVETDTNSVQDEKFVAFSLDKRPELQQ 444 Db 305 LYQIRAHFSGOELNVVQIEENNSKSTYKVGMVETDTNSVQDEKFVAFSLDKRPELQQ 364 Qy 445 PISGAVDPLSDODSVTFNDSCVGESSEHOPDDHUSPSTASPCKRTKSDTEPKSQS 504 Db 365 PISGAVDPLSDODSVTFNDSCVGESSEHOPDDHUSPSTASPCKRTKSDTEPKSQS 424 Qy 505 SGRTSSDDPPICTCSWSDTQDQVLUKGKRLKJAKTELSDIMVSKKKMSPPFCEBD 564 Db 425 SGRTSSDDPPICTCSWSDTQDQVLUKGKRLKJAKTELSDIMVSKKKMSPPFCEBD 484 Qy 565 EQLQLOTDIGSNLEKEKLENSRSLECRSPSPKIKTSLSPTSKUGYSYRDLDLAKKH 624 Db 485 EQLQLOTDIGSNLEKEKLENSRSLECRSPPIKTSLSPTSKUGYSYRDLDLAKKH 544 Qy 625 ASLROTESPDAEPTTLNHAHSSKLVHORLRSRBLKERRARVILQBAARDALAKGNK 684 Db 545 ASLROTESPDAEPTTLNHAHSSKLVHORLRSRBLKERRARVILQBAARDALAKGNK 604 Qy 685 HINTNTATPFCRQLSQDERRQLERARQALIAERSGWMSLPSKGEMAAKLER 744 Db 605 HINTNTATPFCRQLSQDERRQLERARQALIAERSGWMSLPSKGEMAAKLER 664

Qy 745 SKASGDENDWIEIDTMBIFPGFVVGGDSLTLNLENDLTPRQNSKVLVDJKLKKLUBVQP 804 Db 665 SKASG-----EONSKLVDJKLKKLUBVQP 688 Qy 805 QWANSPSAQAQAVTESSEQMKSTEDLRERLQKTERFRNPVVFVSKOSTVRKIQLOS 864 Db 689 QWANSPSAQAQAVTESSEQMKSTEDLRERLQKTERFRNPVVFVSKOSTVRKIQLOS 748 Qy 865 FSOYIENRPEMKRQSIQBUTKKGHEKAATETORKPSDEVLKGPQTSQYVGEA 924 Db 809 ALENESOKOIDTRAALVEKRYLMDTGQNTEEBAMMOSFMLVKKNALIRRMOSSL 868 Qy 985 EKEDLIRRSELLNLBRLAMLAEDWQKTEAQKQRERQQLLDELVALVNLKEDALVRDLDAQ 1044 Db 869 EKEDLIRRSELLNLBRLAMLAEDWQKTEAQKQRERQQLLDELVALVNLKEDALVRDLDAQ 928 Qy 1045 EKOABEBDEBLERTLHQNKQWMAKKEKCVCVQ 1076 Db 929 EKQABEBDEBLERTLHQNKQWMAKKEKCVCVQ 960

RESULT 15  
 ADT70136  
 ID ADT70136 standard; protein; 882 AA.  
 XX  
 AC ADT70136;  
 XX  
 DT 06-MAY-2004 (first entry)  
 DB Human heat mitochondrial protein as a therapeutic target  
 SeqID1942.  
 XX  
 KW mitochondrial; human; screening assay; diabetes mellitus;  
 KW Huntington's disease; osteoarthritis; LMN;  
 KW Leber's hereditary optic neuropathy; LION;  
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
 KW neuroprotective; nootropic; antidiabetic; anticonvulant; antiarthritic;  
 KW osteoprotective; ophthalmological; cryostatic;  
 KW ophthalmic;  
 OS Homo sapiens.  
 XX  
 PN WO2003087768-A2.  
 XX  
 PD 23-OCT-2003.  
 XX  
 FP 04-APR-2003; 2003WO-US010870.  
 XX  
 PR 12-APR-2002; 2002US-0312843P.  
 PR 17-JUN-2002; 2002US-0339987P.  
 PR 20-SEP-2002; 2002US-0412418P.  
 XX  
 (MITO-) MITOKOR.  
 BA (BUCK-) BUCK INST AGE RES.  
 BA  
 PI Ghosh SS, Fahy ED, Gibson BW, Taylor SW, Glenn GM;  
 PI Warnock DR;  
 XX  
 WPI: 2003-845369/7B.

Identifying a mitochondrial target for drug screening assays and for  
 treating diseases associated with altered mitochondrial function,  
 comprising detecting a modified polypeptide in a sample and correlating  
 with the disease.

Claim 1; SEQ ID NO 1942; 180pp; English.

This invention relates to novel mitochondrial targets that can be used  
 for therapeutic intervention in treating a disease associated with an  
 altered mitochondrial function. Specifically, it refers to a method for

identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, encephalopathy, lactic acidosis and stroke (MELAS), myoclonic epilepsy (MECP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytosstatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.

XX  
Sequence 882 AA:

Query	Match	81.7%; Score 4485; DB 7; Length 882;
Best Local Similarity	100.0%; Pred. No. 4e-268;	
Matches	882; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	195 MSKVLYADSSKTEERELDESNNPFPKSPTRPPNNTVPVQBLERERRVKRKAAPPVSP 254	
Db	1 MISKVLYADSSKTEERELDESNNPFPKSPTRPPNNTVPVQBLERERRVKRKAAPPVSP 60	
QY	255 KTGIVLAVENTWAGKOLSTSPKSPRSPVPLRKENAKASQSLVWCKEVTKNTRGKINTF 314	
Db	61 KTGIVLAVENTWAGKOLSTSPKSPRSPVPLRKENAKASQSLVWCKEVTKNTRGKINTF 120	
QY	315 TSWNLGLSFCALIHHPRPDLYKSINPDKKENKKAYDGPASIGISKLRSMDVLLA 374	
Db	121 TSWNLGLSFCALIHHPRPDLYKSINPDKKENKKAYDGPASIGISKLRSMDVLLA 180	
QY	375 IPDGKLTWMTLYQIRAHFSGQELNVQIRENSSIKTYKVGNEYDTNSSVDQSKFYAEL 434	
Db	181 IPDGKLTWMTLYQIRAHFSGQELNVQIRENSSIKTYKVGNEYDTNSSVDQSKFYAEL 240	
QY	435 DLKRREPPELQQPTISGAVIDPSQDDSVFVNDSGGVGESESEHOTPDHLSRSTASPCCRRTS 494	
Db	241 DLKRREPPELQQPTISGAVIDPSQDDSVFVNDSGGVGESESEHOTPDHLSRSTASPCCRRTS 300	
QY	495 DTBPKQSOSGRGSGDPGICNTSDTQAQVLGKRLKAKTELSDLYSDKKDM 554	
Db	301 DTBPKQSOSGRGSGDPGICNTSDTQAQVLGKRLKAKTELSDLYSDKKDM 360	
QY	555 SPPPCIEETDEOKQLTDIGSLNLERKEKLNSRLCRSDPESPIKTSISPTSKLGYS 614	
Db	361 SPPPCIEETDEOKQLTDIGSLNLERKEKLNSRLCRSDPESPIKTSISPTSKLGYS 420	
QY	615 RDIDLAKKKHSILQOTESPDPADRTTLNHADHSSKIVORLLRQBEIKERARVILBOAR 674	
Db	421 RDIDLAKKKHSILQOTESPDPADRTTLNHADHSSKIVORLLRQBEIKERARVILBOAR 480	
QY	675 RDALKAGSKHNTATPCCNROLDQDEERERQRLRERQLTAEANGVYKNSLSESYG 734	
Db	481 RDALKAGSKHNTATPCCNROLDQDEERERQRLRERQLTAEANGVYKNSLSESYG 540	
QY	735 EMARKLKERSKASGDENDNEIDTNEETPFGVVGGEDELTLNLENDIDTPCNSKLVDL 794	
Db	541 EMARKLKERSKASGDENDNEIDTNEETPFGVVGGEDELTLNLENDIDTPCNSKLVDL 600	
QY	795 KLKCLLEVOPQVANSPSSAQAVTTESSQDMSGTEDLRTERLQKTERFRPNUVFSKD 854	
Db	601 KLUKKLLEVOPQVANSPSSAQAVTTESSQDMSGTEDLRTERLQKTERFRPNUVFSKD 660	
QY	855 STVRKTQLOPSQSOYIENREMMKRSIERTDKKGNEKAITETORKSEDEVLNKGKD 914	
Db	661 STVRKTQLOPSQSOYIENREMMKRSIERTDKKGNEKAITETORKSEDEVLNKGKD 720	
QY	915 TSQYNGELLALENEMQKQIDTRALVEKLRLYMDTGRNTEERAMQEWFFMLVJKQAL 974	
Db	721 TSQYNGELLALENEMQKQIDTRALVEKLRLYMDTGRNTEERAMQEWFFMLVJKQAL 780	
QY	975 IRRNQNLISLKEHDLERSYELARELRLAMLAEDWQKTEAKQKREQLLIDELVALVNR 1034	

Db 781 IRRNQNLISLKEHDLERSYELARELRLAMLAEDWQKTEAKQKREQLLIDELVALVNR 840  
QY 1035 DALVRDLOQEKQREBEDHLERTLEQKGMKAKRECVLQ 1076  
Db 841 DALVRDLOQEKQREBEDHLERTLEQKGMKAKRECVLQ 882

Search completed: May 20, 2006, 17:09:12  
Job time : 207 secs

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GeScore Version 5.1.8

run on: May 20, 2006, 17:14:58 ; Search time 53 Seconds

maximum protein - protein search, using sw model

total number of hits satisfying chosen parameters: 650591

minimum DB seq length: 0

maximum DB seq length: 200000000

post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

database : issued Patents AA:\*

1: /EMC\_Celerra\_SIDS3/podata/2/iaa/\_5\_COMBO.pep:\*

2: /EMC\_Celerra\_SIDS3/podata/2/iaa/\_6\_COMBO.pep:\*

3: /EMC\_Celerra\_SIDS3/podata/2/iaa/\_7\_COMBO.pep:\*

4: /EMC\_Celerra\_SIDS3/podata/2/iaa/\_H\_COMBO.pep:\*

5: /EMC\_Celerra\_SIDS3/podata/2/iaa/\_PCTUS\_COMBO.pep:\*

6: /EMC\_Celerra\_SIDS3/podata/2/iaa/\_RE\_COMBO.pep:\*

7: /EMC\_Celerra\_SIDS3/podata/2/iaa/\_backfile1.pep:\*

scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
searched: 650591 seqs, 87530628 residues

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

result No.	Score	Query Length	DB ID	Description
1	5486	99.9	1076	2 US-09-976-594-889 Sequence 889, App
2	326.5	5.9	3433	2 US-09-530-092-1136 Sequence 1136, Ap
3	307.5	5.6	2141	2 US-09-949-016-10918 Sequence 10918, A
4	301.5	5.5	3433	2 US-09-949-016-10918 Sequence 10918, A
5	296	5.4	61	2 US-09-949-016-10918 Sequence 10918, A
6	291.5	5.3	2154	1 US-09-841-349-4 Sequence 349, Ap
7	291.5	5.3	2154	1 US-09-431-1894-4 Sequence 1894, Ap
8	291.5	5.3	2364	2 US-09-530-1243 Sequence 1243, Ap
9	286	5.2	2388	2 US-09-655-795-2 Sequence 795, Ap
10	285	5.2	1026	2 US-09-949-016-6777 Sequence 6777, Ap
11	285	5.2	1034	2 US-09-949-016-10870 Sequence 10870, A
12	283.5	5.2	153	2 US-09-270-767-42273 Sequence 42273, A
13	276.5	5.0	912	2 US-09-664-958-8 Sequence 958, Ap
14	274	5.0	883	2 US-09-664-958-8 Sequence 958, Ap
15	270.5	4.9	2008	2 US-09-091-501B-8 Sequence 501B, Ap
16	270.5	4.9	2186	2 US-09-949-016-10828 Sequence 10828, A
17	270.5	4.9	2349	2 US-09-538-092-914 Sequence 914, Ap
18	264	4.8	1078	2 US-09-248-796-20284 Sequence 20284, A
19	264	4.8	2662	2 US-09-955-684B-31 Sequence 684B, Ap
20	262.5	4.8	2663	2 US-09-530-1252 Sequence 1252, Ap
21	261.5	4.8	2375	2 US-09-538-092-1131 Sequence 1131, Ap
22	261	4.8	630	2 US-09-248-796A-20275 Sequence 20275, A
23	258.5	4.7	1093	5 PCT-US93-0377-1 Sequence 1, Ap
24	258.5	4.7	1093	5 PCT-US93-0377-1 Sequence 1, Ap
25	256	4.7	1976	2 US-09-538-092-1078 Sequence 1078, Ap
26	256	4.7	1082	2 US-09-134-001C-3159 Sequence 3159, Ap

**RESULT<sup>1</sup>**

; Sequence 889, Application US/09976594

; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09-976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO: 889

; LENGTH: 1076

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE: misc\_feature

; NAME/KEY: misc\_feature

; OTHER INFORMATION: Incyte ID No. 6673549 5202390CD1

US-09-976-594-889

Query Match 99.9%; Score 5486; DB 2; Length 1076; Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0; Matches 1075; Conservative

QY 1 MKQYASPMPTOTDVKPKPLSKVVSALQFSLSCIREGKATDEMDQMSLAVLSMKQ 60

Db 1 MKQYASPMPTOTDVKPKPLSKVVSALQFSLSCIREGKATDEMDQMSLAVLSMKQ 60

QY 1 ADIGNLDDEDDDDENRVEEKAATIETLNKLNFLEAKDLATVNSNPPDDPA 120

Db 61 ADIGNLDDEDDDDENRVEEKAATIETLNKLNFLEAKDLATVNSNPPDDPA 120

QY 121 AEIAPFGDPDSEPIETETASPRKTESDFSTFNNSTPFPKVOTPOYLNPDEPEARTIKOS 180

Db 121 AEIAPFGDPDSEPIETETASPRKTESDFSTFNNSTPFPKVOTPOYLNPDEPEARTIKOS 180

QY 121 AEIAPFGDPDSEPIETETASPRKTESDFSTFNNSTPFPKVOTPOYLNPDEPEARTIKOS 180

Db 121 AEIAPFGDPDSEPIETETASPRKTESDFSTFNNSTPFPKVOTPOYLNPDEPEARTIKOS 180

QY 181 PPSTKRNTRPDMSKLYADDSKTRFELDSNPPYEPKSTPPNNVNPKOLETER 240

Db 181 PPSTKRNTRPDMSKLYADDSKTRFELDSNPPYEPKSTPPNNVNPKOLETER 240

QY 181 PPSTKRNTRPDMSKLYADDSKTRFELDSNPPYEPKSTPPNNVNPKOLETER 240

Db 181 PPSTKRNTRPDMSKLYADDSKTRFELDSNPPYEPKSTPPNNVNPKOLETER 240

QY 241 RVKKAPAPPVLSPTKGVLNENTVAGKDLSTSPKPSP1TPSPVLRKPNASQSLVWCKE 300

Db 241 RVKKAPAPPVLSPTKGVLNENTVAGKDLSTSPKPSP1TPSPVLRKPNASQSLVWCKE 300

QY 301 VTKNYGVKINTTSMWNLGLSHCATLHFRPLIDYKSNPDKKENKKADGFASTG 360

Sequence 7309, Ap

Sequence 2964, Ap

Sequence 11, Ap

Sequence 16, Ap

Sequence 10872, Ap

Sequence 16333, A

Sequence 11433, A

Sequence 6507, Ap

Sequence 1077, Ap

Sequence 4, Ap

Sequence 11, Ap

Sequence 2, Ap

Sequence 9, Ap

Sequence 11, Ap

Sequence 4, Ap

Sequence 4, Ap

Sequence 1879, A

Sequence 7561, Ap

Sequence 11433, A

Sequence 6507, Ap

Sequence 1077, Ap

Sequence 4, Ap

Sequence 11, Ap

Sequence 2, Ap

Sequence 9, Ap

Sequence 11, Ap

Sequence 4, Ap

Sequence 4, Ap

Sequence 1879, A

Sequence 7561, Ap

Sequence 11433, A

Sequence 6507, Ap

Sequence 1077, Ap

Sequence 4, Ap

Sequence 11, Ap

Sequence 2, Ap

Sequence 9, Ap

Sequence 11, Ap

Sequence 4, Ap

Sequence 4, Ap

Sequence 1879, A

Sequence 7561, Ap

Db 301 VTKYVGRVKINTNFTSWRNGLSFCALIHFPRPLIDYKSINPODIKENRKAYDGASTG 360  
 Qy 361 ISRLLEPSDMVLLAIPDKLTWMTYQIAHPSQBLNVOIEENNSKSTYKVNEYDT 420  
 Db 361 ISRLLEPSDMVLLAIPDKLTWMTYQIAHPSQBLNVOIEENNSKSTYKVNEYDT 420  
 ; US-09-538-092-1136

; FEATURE: misc\_feature  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (0).-(0)  
 ; OTHER INFORMATION: Polypeptide Accession Number P46939

Query Match 5.9%; Score 326.5; DB 2; Length 3433;

Best Local Similarity 19.8%; Pred. No. 2.6e-12; Mismatches 336; Indels 303; Gaps 37; Matches 197; Conservative 159; MisMatches 336; Index 148

Db 421 NSSVSDQEKKYELSDKREPLOOPIGAVDIFLSODDSVFUNDGVGBESBESHOPTDDHL 480  
 Db 421 NSSVSDQEKKYELSDKREPLOOPIGAVDIFLSODDSVFUNDGVGBESBESHOPTDDHL 480

Qy 481 SPSTASPYCRRTKSDTEPQKSSQSGRTSGSDDPGICCSNTSDSTAQVILGKRULKAETL 540  
 Db 481 SPSTASPYCRRTKSDTEPQKSSQSGRTSGSDDPGICCSNTSDSTAQVILGKRULKAETL 540

Db 541 BLSDLVSKPSKKDNPSPFCEBTBKQLOLIGNSLEGEKLNSLSCRSPEPIK 600  
 Db 541 BLSDLVSKPSKKDNPSPFCEBTBKQLOLIGNSLEGEKLNSLSCRSPEPIK 600

Db 601 TSLSPTSKGYSISRDLJAKKHSRQTESDADRTLNHDHSKIVQRHLSRQE 660  
 Db 601 TSLSPTSKGYSISRDLJAKKHSRQTESDADRTLNHDHSKIVQRHLSRQE 660

Qy 661 BLKERRARVILLEQARDAAKAGNAKHNTATPPCNROQSQDQBERRQLRERAROLAE 720  
 Db 661 BLKERRARVILLEQARDAAKAGNAKHNTATPPCNROQSQDQBERRQLRERAROLAE 720

Qy 721 ARSGVTKMSLPSKGEMAAKLUKERSKASDENDNIEIDTNEBPEGFVUGGBLNTEN 780  
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Qy 781 DLDTPEONSKVLDIJKKULBVQOVANSPSAQAVTESSEODMKSTEDIRERIQK 840  
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Qy 841 TTERFRNPVPSKOSTVRKTQLOFSQYIENREPMKORSIQEDTKGSNEKEKAIITERQ 900  
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Qy 901 KPSDEVLVNGFKOTSOVYQVGLAALENQKOIDTRALVEKRYLMDTGRTNTEEAM 960  
 Db 901 KPSDEVLVNGFKOTSOVYQVGLAALENQKOIDTRALVEKRYLMDTGRTNTEEAM 960

Qy 961 MQEPMFLVNLVKNALIRMQLSLIKEHDLRREYLNLRLMATEDWQKTAQKRB 1020  
 Db 961 MQEPMFLVNLVKNALIRMQLSLIKEHDLRREYLNLRLMATEDWQKTAQKRB 1020

Qy 1021 QLIDDELVALVNLVKDALVERDLDQEQKQABEBDEHLERTLEQNKGKMKKEKCVTLQ 1076  
 Db 1021 QLIDDELVALVNLVKDALVERDLDQEQKQABEBDEHLERTLEQNKGKMKKEKCVTLQ 1076

RESULT 2  
 US-09-538-092-1136  
 Sequence 1136 Application US/09538092  
 Patent No. 6753314  
 GENERAL INFORMATION:  
 APPLICANT: Giot, Iolic  
 APPLICANT: Mansfield, Traci A.  
 TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
 FILE REFERENCE: 15966-542  
 CURRENT APPLICATION NUMBER: US/09/538,092  
 CURRENT FILING DATE: 2000-03-29  
 PRIOR APPLICATION NUMBER: 60/127,352  
 PRIOR FILING DATE: 1999-04-01  
 PRIOR APPLICATION NUMBER: 60/178,965  
 PRIOR FILING DATE: 2000-02-01  
 NUMBER OF SEQ ID NOS: 1387  
 SOFTWARE: CuraprotSeqFormatter Version 0.9  
 SEQ ID NO 1136  
 LENGTH: 3433  
 TYPE: PRT  
 ORGANISM: Homo sapiens



208 TERLEHAFSKAHTYLGIEKULDPEDAVHLXXXKXXXXXVLPQOVTIDAIREVE 267

383 TLYIQRAHSGCBLAV-- VOLENSSKSTYKVNEYETNSIDQEKYAEASLKE 439

268 TLPRTYKKEEEBTHIQSAVLABEGSP-----RAATPSTVEMDLSQIALE 319

440 PELOOPISGAVDELSODDSVFVNDSVGUGESSESEHOPDILSPSTASPYCRRTKSDTEPQ 499

320 EULTMILSBDTFOQDD---ISD-VEEKEQFATHERMELTA-----H 362

500 KSIQPSGRSGSD- DPGICSNSTSQAQ---VILGKBRLLKATL-----ISDLYVSD 549

363 QSSVGSVLQAGNQLMTGTLSEEFIOBOMTUNARWEALRVESMEROSRLHDALME 422

550 KKK---DMSPPRIFETDEKLQDNLIGSLE - KEKLNRSRSCRSPEPSPIKTS 604

423 QKQDQQLSWLAITTEQKMESEPLGDLSPQXLUQEHKSQNDLAEQ-VKVNLT 491

605 ----- PTSKGYSRSRDLDAKCKHASLHQ----- 629

482 HMMVIVDENGESATALELDQLOKJGGERWTAVCRTEETERWNLQIISTIMQELBQCL 541

630 ---TESPDADRT-TLNHDHSSKIVQHLLSQEELKERARVILEQARRDAALKAGNK 684

Db 542 EAMLEKEEALNKVQTSNFKDQKELLSVSVERLATIKAEDMEMKRTLDQIS-----EIGD 596

685 HNTVATPENROQSDDQBERR---QLERAROLIAEARSGVRSBPLSPYGMARE 739

597 VQQLISNPRAKSKKNSDSEBLTORQDSLVRLEDSSNOTQAVAKLGMNSQIPQDKLLEV 656

740 KLKERSKAS-----GDENDNIEIDNEPEPEGFVUGGGD-----E 774

QY 715 IKEMKMQTSEMREKIKALE-KERQERPR-ADEBNQGQILVEQ-----MGKEGLP 765

657 HVRIKGWVKPKQELPPQPKRQIHVDI--EAKKFDASIBALNWLKWKAQTR 714

775 LTNLENDLDTPEQNSKLVDLKLUKEVOPQVANSPPSAQAVTESSEBQDMKSGTEDIR 834

Db 835 TER---LOCTTERPN-----PVFSKOSTVTKTQLOFSFOYENRPMKRS 880

766 TEIKNVLBKVSSBKNVQSHLEDLBRKIQLOQDINAYFKQDDBLKVTKTBWKITS 825

881 IQRDTK-----KGENBEGAITTORKESSEDEBLANKGP----- 912

826 ISESRQSLPSLKSOCORELNTLIGLHPKLEMARSCALSMSOPASAPDVQRGDFSLGR 885

913 -----KDTQSVVGEELAALEHEQKQIDTRALMVERKLYMDTGRENTE----- 955

886 YQAVQEAVEDRQH-----LENLKGCPGHAVL-EITKTIKDVLANDSENKAQVSLAV 936

956 -----EBRMMQWFMPLNKTQKQNLIRRMQSLIEK--EHDJERRYHNRLR 1002

937 LNDLAKVEKALOEKRTLDE--ILENQKPAHLKJAEETKALEKVNHPDFEKLYQBFDDVQ 994

1003 AMLAEDMOKTEAQKREGULDILV-----ALVNKRDLVLDQAQKQAEED 1052

995 G----KRNKLVKUQSKDULHBLTALTRAFASTDSTVIEKWDGVKDPLMKQQAQGDD 1049

QY 1053 EHBLRTBLEQ 1061

Db 1050 AGIQRQDQ 1058

RESULT 6

US-08-841-349-4

; Sequence 4, Application US/08841349B

; Patent No. 5955594

; GENERAL INFORMATION:

; APPLICANT: MISURA, LOPA

; TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT. . .

; FILE REFERENCE: XW/P0470US0

; CURRENT APPLICATION NUMBER: US/08/841,349B

; CURRENT FILING DATE: 1997-04-30

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 2154

; TYPE: PRT

; ORGANISM: Mus musculus

US-08-841-349-4

Query Match 5.3%; Score 291.5; DB 1; Length 2154;

Best Local Similarity 20.3%; Best Match 146; Mismatches 326; Indels 291; Gaps 38;

Matches 194; Conservative 146;

QY 287 KPNMASQSLVWQKMTGKTYGPNINHFTSMQGMFANLHHKRPDLIDYKSLNPDIK 346

Db 159 KCKSAKDALLWQKMTGKTYGPNINHFTSMQGMFANLHHKRPDLIDYKSLNPDIK 318

QY 347 ENHKAYD-GFASIGIRLPSLSDMVLAIPPLTVWYQOIRAHSGQBLNVO----- 401

Db 219 YNLQNAENLAECHGLTQKLDPE-1SDVHPDKSITYVYVYHFSKMKALAVEKRI 277

QY 402 -IEENSSKSTYKVNEYET-----DTNSV 424

Db 278 GKVLDAETEMKIEYETLADLLENIEQTIIILNNRKPAVLVQQLQAFNTVTRV 337

QY 425 DQKPFYABLSDIK-----REPELQOPTSGAVDLSQDSDSVFNDS 464

RESULT 5

US-09-513-999C-7173

; Sequence 7173, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J. B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

CURRENT APPLICATION NUMBER: US/09/513,999C

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: PatentIn.pm

SEQ ID NO 7173

LENGTH: 61

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: UNSURE

LOCATION: 15

OTHER INFORMATION: Xaa=Ile or Lys or Arg or Thr

FEATURE:

NAME/KEY: UNSURE

LOCATION: 39

LOCATION: 17

OTHER INFORMATION: Xaa=Asp or Glu

FEATURE:

NAME/KEY: UNSURE

LOCATION: 39

OTHER INFORMATION: Xaa=Asp or Glu

US-09-513-999C-7173

Query Match 5.3%; Score 291.5; DB 2; Length 2154;  
 Best Local Similarity 20.3%; Pred No. 2.8e-10; Matches 194; Conservative 146; Mismatches 326; Indels 291; Gaps 38; Matches : 194; Conservati 146; Mismatches 326; Indels 291; Gaps 38;

Db 338 BKKPKPTEKGNLRLVLPATOSKMRANNQKVMPRECKLISDINKAWERLK----- 388  
 Qy 465 GVGESSESHQTPDDHSPSTASPCTPCRKTSTPQSQQSSGR----TSGSDPGICS 518  
 Db 389 --AEHERELARNLRLRQEKEKQLAQRFDRAKMRTEWLNRQVLSQDNGFDPDAVEA 446  
 Qy 519 NTDSQA-----OVLGKGRKLAKT----- 542  
 Db 447 ATKKHEAETIAAYSERVOAVAVARBLEENYHDKRITARKDNVIRLWEYLBLRA 506  
 Qy 543 -----SLVYSDKKDMSPPICEB-----TDOKLOTIDS 575  
 Db 507 RRQLEMLNLGQKIFQEMLYIMWDMDMKVLLSQDYKGHLGVEDLQKHALVEADAI 566  
 Qy 576 NLEKKEKLENSSLECSRDP--SPIKKTSI-SPTSKLGYSYSRDLDAKKKHSASRQT-- 630  
 Db 567 QAEVRGYNASAQKEPATDGYKPCPQVDRVARMEPCYQELCOLAARRARLESRR 626  
 Db 631 -----ESPDADRTLNHADHSKIVQ-HRLSLR---OBELKEARVILEQAR 674  
 Qy 627 LWKPFWEMABEGWIRKEKEKILSSDDYKGDTISVRLSKHRAPEDMSGSG-HFEOAI 685  
 Qy 675 RDAALKAGNKINTDATPFCRNOLSDQCBERRRQLRERARQLLEARSGTKMSLPSVG 734  
 Db 686 KEGEDMIAEEH-----FGSEKIRRTITYRBOWANL--BOSAIRKRLBEE-- 729  
 Qy 735 EMAEKKERSKASGDENDNIEIDTNEBIPGFVVGGS 733  
 Db 730 ---ASLHQFOAADDIDAMWDLIKIVSNND--GHDRYSTOSLVKHKDVABEITNC 783  
 Qy 779 ENDLT-PEONSKLVDLKLKLULEVPOV-ANSPSSAAQKAVTESSEODMKSGTEDRTE 836  
 Db 784 RPTDITLHEQASAL-----POAHAEPSDVKGRLAGIEERCKEMABLTR-LRKQ 830  
 Qy 837 RLOKTERFRPNPVFSKOSTRKTOLOFSQYENRPEMKRQRSIQEFTKGNEKAIT 895  
 Db 831 ALQDTALYK--MFS-----BADCBLWIDEKOMLNNOIPE----- 866  
 Qy 897 STORKPSDEBLVKNGFKDTSQVVGGLALENEOKOIDTRAALVEKRLYLMGTNTREE 956  
 Db 867 ---KLBDEJVIORFE-----SLPEPMNNQASRVAVNQIROLMINGHPBK 911  
 Qy 957 EAMMOB-----WF----MLVNKGNALTRMNQSLLEKEHDLLRYELRNRELAMLA 1007  
 Db 912 BIRAOQDKLUNTRWSQFRELVDRKDAL--LSALSI-----QNYHLCNETKSCIR- 959  
 Qy 1008 EDWOKTEAQKERRQEQLLD--ELVALVNKRDLVRLDQE-----KOAB-EDEH 1054  
 Db 960 ---EKTKVIESTODLGNDLAGVMALQCKLTOMERDVLVAIEAKLSDLQKEAKLESEH 1013  
 RESULT 7  
 US-09-431-184A-4.  
 Sequence 4, Application US/09431184A  
 ; Patent No. 6642362  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MISHRA, LATA  
 ; TITLE OF INVENTION: GENES CODING FOR EARLY LIVER DEVELOPMENT...  
 ; CURRENT APPLICATION NUMBER: US/09/431,184A  
 ; CURRENT FILING DATE: 1999-11-01  
 ; PRIOR APPLICATION NUMBER: PCT/US98/08656  
 ; PRIOR FILING DATE: 1999-04-30  
 ; PRIOR APPLICATION NUMBER: US 08/841,349  
 ; PRIOR FILING DATE: 1997-04-30  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn version 3.0  
 ; SRQ ID NO 4  
 ; LENGTH: 2154  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-09-431-184A-4

RESULT 8  
 US-09-536-092-1243  
 ; Sequence 1243, Application US/09538092

Patent No. 6753314  
 GENERAL INFORMATION:  
 APPLICANT: Giot, Loic  
 APPLICANT: Mansfield, Traci A.  
 TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
 CURRENT APPLICATION NUMBER: US/09/533,092  
 CURRENT FILING DATE: 2000-03-29  
 PRIOR APPLICATION NUMBER: 60/127,352  
 PRIOR FILING DATE: 1999-04-01  
 PRIOR APPLICATION NUMBER: 60/178,965  
 PRIOR FILING DATE: 2000-02-01  
 NUMBER OF SEQ ID NOS: 1387  
 SOFTWARE: CurapateSeqFormatter Version 0.9  
 SEQ ID NO: 1243  
 LENGTH: 2364  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (0)..(0)  
 OTHER INFORMATION: Polypeptide Accession Number Q01082  
 US-09-538-092-1243

Query Match 5.3%; Score 289.5; DB 2; Length 2364;  
 Best Local Similarity 19.3%; Pred. No. 4.2e-10; Mismatches 369; Indels 331; Gaps 43; Matches 208; Conservative 171; Mismatches 369; Indels 331; Gaps 43;

QY 287 KPNASQSLUWCKEVTKMYRGKINTFTSWRNGLSPCATLHHFRPDLDYKSINPQDTK 346  
 Db 172 KKSADKALLWICMKTAGYPNVNINFTSWRNGLSPCATLHHFRPDLDYKSINPQDTK 346  
 QY 347 ENNKAYD-GFASIGISRLPEPSDMVLAIPDKUTVMTYQIYRAHFSQELNMQ-- 401  
 Db 232 YNLQNAFPNLAEQHLGLTLDPE-LSVDPHDPEKSITTVVTTYHYFSKOMKALAVEGRI 290  
 QY 402 -IRENSSKSYSTKYVGYET---DTNSAV 424  
 Db 291 GKVLDAIASTEKMTKRYESLASDILLEWIEBOTITLNRKFAFANSLVGVQQQLQAFNTYTV 350  
 QY 425 DQEKFYAEFLDLK-----REPELQPIGSAVDELSQDDSVFVND 464  
 Db 351 EKPKRPTEKGNLLEVLTIQSOMRANNQKYMPPREGKLSDINTKAWERJEK----- 401  
 QY 465 GVGSESEHOTPDHLSPLSPSTASPVCRTKSDTEPOKSOSSGR-----TGSDDPGICS 518  
 Db 402 -AHEERELARNLIRQEKLEQKLLRDRKAAMRBTWILSENQRLVSQDNFGFDLPAVERA 459  
 QY 519 NTDSQAA-----QVLUKGKRKAET-----LEL--- 542  
 Db 460 ATKGHEAIEDTAAVEEROVAVAVARELAENHDIKRITARKDNVIRLWVEYLILRA 519  
 QY 543 -----SDJYVSDKKKMPPPFICE-----TDEQKQTDIGS 575  
 Db 520 RPROLEMNGLGOKIFOEMLYMDRNDDEMKTIVLUSQDGKHLGVEDLQKHTLVEADIGI 579  
 QY 576 NEGEKLEMSRSLRCSRSDPR--SPIKRTSI-SPTSKLGYSRSRDLJACKKKHSRLQT-- 630  
 Db 580 QAERVGCVMASAQREATDSRGKFCDPQVIRDRVAHMERCYQELCQLAARRABLESRR 639  
 QY 631 -----ESPDADRTLNHADHSKTVQ-HRLUSR---QEEUKERARYLSSQR 674  
 Db 640 LWKPFWMABEGWIREKEKSLSSDYGKFCDPQVIRDRVAHMERCYQELCQLAARRABLESRR 698  
 QY 675 RDALKAGKHK---NTNTATPCNQLS--DQDEBRQRRLERA-RQLEARS-- 723  
 Db 699 KEGDMAEEHFGSEKIRITIYTRBQWANLQSAIRKRLERASLHOFQADADDIDA 758  
 QY 724 -----GVMSLPSYGEAMAUKERSKASGDENDNIE-IDTNEB---IPE---- 765  
 Db 759 WMLILKIVSSDWGDEVTSQSLVKKHDAEARIANTPTDLOTHEQASALQFEHASSP 818  
 QY 766 --GFVVGGGD-----BLTNL-----NDLDTP 785

RESULT 9  
 US-09-635-795A-2  
 Sequence 2, Application US/09/635795A  
 Patent No. 6808893  
 GENERAL INFORMATION:  
 APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
 APPLICANT: ROHSTEIN, Jeffrey D.  
 APPLICANT: JACKSON, Mandy  
 APPLICANT: LAN, Glen  
 APPLICANT: ORLOV, Irina  
 TITLE OF INVENTION: GLUTAMATE TRANSPORTER ASSOCIATED PROTEINS AND METHODS OF USE THEREOF  
 FILE REFERENCE: JH01650-2  
 CURRENT APPLICATION NUMBER: US/09/695,795A  
 CURRENT FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: US 60/161,007  
 PRIOR FILING DATE: 1999-10-23  
 PRIOR FILING DATE: 2000-05-22  
 NUMBER OF SEQ ID NOS: 22  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 2  
 LENGTH: 2388  
 TYPE: PRT  
 ORGANISM: Rattus  
 US-09-695-795A-2

Query Match 5.2%; Score 286; DB 2; Length 2388;  
 Best Local Similarity 22.0%; Pred. No. 7.3e-10; Mismatches 320; Indels 246; Gaps 41; Matches 200; Conservative 143; Mismatches 320; Indels 246; Gaps 41;

QY 287 KPNASQSLUWCKEVTKMYRGKINTFTSWRNGLSPCATLHHFRPDLDYKSINPQDTK 346  
 Db 175 KKSADKALLWICMKTAGYPNVNINFTSWRNGLSPCATLHHFRPDLDYKSINPQDTK 346  
 QY 347 ENNKAYD-GFASIGISRLPEPSDMVLAIPDKUTVMTYQIYRAHFSQELNMQ-- 405  
 Db 235 YNLQNAFPNLAEQHLGLTLDPE-VNDQDPEKSITTYVATYHYFS--KOKALAVE-- 289  
 Db 406 SSKSYTGYENYEDTNSVDOQEKFYAEFLDKRPELQPIGSAVDELSQDDSVFVND 465  
 Db 290 -GRIGKGLDHAMEAHLV--EYEVESL-----LOWBOTIGTP-NDRQ 332  
 QY 466 VGSESEHOTPDHLSPLSPSTASPVCRTKSDTEPOKSOSSGRTSGSDDPGICNTSTQA 525

Db 333 LANS-----LSGVQNQLOSPNSRT--VEKPP--KFKEKGNL 365  
 Qy 526 QYLL-----GKRLRKAETBLISLUVSKDKDMSPPPICRETDECKLTDIGS 575  
 Db 366 EULLPFTIOSKURANNOVYTRREGRLISDINKAWERLEKA----EHEBELALRT---E 416  
 Qy 576 NLERKCLENSRSLECRSDPSSPIKITSLSPTSKLGYSYSDIDLAK----KXHASLRQT 630  
 Db 417 LIROKLB--OLAARFDKAMRETWLSENORLVSQDNFGELAVEAVRKHAI-ET 472  
 Qy 631 ESDPDADRTTINAHADHSKIVOH----RLJSRQB----LKB----RARVIL--- 670  
 Db 473 DIVAVSGRVDAVAAELAEHYDIDIKRIMARONVARLMDPLKEMVAARRERULINIE 532  
 Qy 671 -----EQARRDAAALKAGNKHNTN- 688  
 Db 533 LQKVFDQLYLAMDWMAMEMKGRLQSOPGLKHLAGVEDDLQHLVELVERDIAVQEVRAVSA 592  
 Qy 689 TATPPCN----RQLSDQDEER--RRQJERAROLIAERASGWOMSE---LPSYGE 735  
 Db 593 SALRCPDPGKEYRPGPQPVSRATEDSYEALEGHLAATRARIRESRULWLTWEGV 652  
 Qy 736 MAEAKLKERSKASGBENDNIBIDTNBEPBGFVVGGDELNLNDL---TPEONSK 790  
 Db 653 ARAWREQQHILASET----GRDITGVRLINKHTALRGEMSGR 693  
 Qy 791 LVDLKLKKLUEVPOVANSPSSAAOKAVTESS-ODMKSGTEDLTERLQKTTFRNPV 849  
 Db 694 LGPLKL--TLEQGOOLVAEGHGANOASTRALQAOQWERLALAEERAOQLAQ-ASLY 750  
 Qy 850 VPSKOSTVTKTQLOFSQYIENRPEM----KQRSIQDPTKKGONERKAITE 898  
 Db 751 QFOADANDMERMALWVLALUVS--PEVGHDFESTOALARALEBEIRAMRPTDALB- 808  
 Qy 899 ORKPSBDEVELNGKFDTSQVWGBELAALENEOQOIDTRAALVEKRLRYLMGTGRNTEEE 958  
 Db 809 ----QAAALFPALSHTEP-WQGRIFTLEQHTEQIARA----GERARAJE 849  
 Qy 959 AMMOEWPMI-----VNKNALIRRMNOLSLKEHD--LERRYSELNREBMLA 1006  
 Db 850 ALAPFTYMLSEAGAGLWEEKB--QWLNGALPERLEDPEVWVQRFETEPENNALLA 906  
 Qy 1007 IEDPKTTRAKRKSOLL----LDELVAL--VNKRDLVRLDAQEKO----EEBD 1052  
 Db 907 ---RITAVSDIABOLLIKASPPGKDRIGTOBQLNQWOFRSLLAGKKALTALSATION 962  
 Qy 1053 EHRLTLEQ 1061  
 Db 963 YHSLCTETQ 971

RESULT 10  
 US-09-949-016-6777  
 ; Sequence 6777, Application US/09949016  
 ; Patent No. 681239  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILING REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 6777  
 ; LENGTH: 1026  
 ; TYPE: PRT

; ORGANISM: Human  
 ; US-09-949-016-6777  
 ; Query Match 5.2%; Score 285; DB 2; Length 1026;  
 ; Best Local Similarity 21.2%; Pred. No. 2.7e-10;  
 ; Matches 242; Conservative 153; Mismatches 363; Indels 384; Gaps 58;  
 ; Gap Open Cost 10; Gap Extension Cost 3;  
 ; Scores 116 DDP--DAEELNPFGDP-----DSEEPYTETASPRKTFDSFYNSYNPKEVOTPQYL 165  
 ; Db 79 DGPRSDSVEGSPFRPPSHFSAVFDEDKPIASSGT----YNLDFDNIELVDTFQTL 130  
 ; Qy 166 NP-----FD-----EPEA 173  
 ; Db 131 EPRASDAKQNEOGKUNTRKSTDSVPISKSTSRLSLSQASDPDGASSGNPEAVALAPA 190  
 ; Qy 174 FVTIKDSPPOSTR-KNIRPVDMSKYLADSSKTBEBELDSNPFYPMKSTPPPNLV-- 230  
 ; Db 191 YSTGSASSSTLKRTPKPPSICK----KOPTKPKTETPPYKETQQEPDERSLIPS 243  
 ; Qy 231 --NPVOBLETERVRVKAPR-----PVLSPKT-----GVLN-----E 261  
 ; Db 244 GENLASETKTE-SAKTEGFSPALLEBTPLPEAVGPKAACPDLDSBSABGVVPPASGGGRVQ 302  
 ; Qy 252 NTVSAGK--DLSTSPKPEP--PAPVIGKPNASQSLJWCKETVKNYVGUKLNTFTSW 317  
 ; Db 303 NSPPVGRKTULPTTAPEAGEVTPRSDGKGDPSAKGLSV--RUEFDYSDK----SS 354  
 ; Qy 318 RNLGSPCAILHHFRDLITYKSLNPQDIKENNKAYDFASIGISRLLEPSDMVLLAIPD 377  
 ; Db 335 -----INQDENPPPTKIGK-----PVATMPLEPRK--MKTPE 387  
 ; Qy 378 KLTWMTYXOIRAHPSQBLANVVOZEEENNSKSTYKVGYETDTNSVDOBK--YALSD 435  
 ; Db 388 KLD-NTPASPR--SPARPNDFI--AKGTY--TFDID--KWDPPNPNFNPSSTSK 433  
 ; Qy 436 LKRPELLOPISGAVDEQSDDSYFVNISGVGSESEHOTPDDILSPASTPYCRTKD 495  
 ; Db 434 MQESPKLPQ-----OSVNFDPD--TCDBSVDPEPKNSKTP 466  
 ; Qy 496 TEQKS----QOSSGRITSGSGDDPGICNTDSQAQVULGKRLKAKTELSDLVYSD 549  
 ; Db 467 SSRSPKSPASPEIAPSAMBRANGVQDGL--NKPARK-----KTPKLKDTPFRV--SP 515  
 ; Db 516 KRSPSLSDPPSQQDPPTAATFETPPVISAUVHATBKEKLAVTNQRWTCTWD---LEADQ 571  
 ; Qy 583 ENSISLCISCDPSSPIKITSL-STPSKLGYSYRDLDAKKKHAISLQTESPDDADRTL 641  
 ; Db 572 DYPQP---SDLSTFVNETKFSSPTEELDYNRSYEIBMEKGSSLPODDAP----- 620  
 ; Qy 642 NHADHSKIVOHRLRSQBELKERARVILQVARDALAKGNKHNINTATPPCNURQLSDQ 701  
 ; Db 621 -----KQALYMFDTSOESPKTSSPMSBP-----CS 654  
 ; Qy 702 ODEERRQRLERA----RQLTAAEASGVKMSLPSYGMAMEKLRKERSKASGBEND 754  
 ; Db 655 SFERSTEALVNTAAKNQHPVPRGLAPNQSHLQVPEKSSOKLEAMGL----GTPSRA 707  
 ; Qy 755 IEDTNEKEPEGFVGGDELTMNDL-----DTPEONSKVNDLKURKLGIVRQ 803  
 ; Db 708 IEITA---PEGSFASADALLSLRHALHPVSLGAQDYLSPDLASKNPPFLPAOKLQBEEFA 763  
 ; Qy 804 PQVANSPSSAAOKAVTESSQDMKSGTSDLRTSRLQKTT----TERFRNP--WVFSK- 853  
 ; Db 764 IMRBLAKLQARQALASHSHQDRAEAMPTDVISISKALYSLRIGTAAVEKPGILFQP 823  
 ; Qy 854 --DSTVTKTQLOFS-----QYENRPNPKRQSIQBDTKGMBEKAATETORK 901  
 ; Db 824 DLDLQIARABITKERVSEWKYKESRREVMKIVARVEK----TIAQ 873  
 ; Qy 902 PSBEPDVNLNGKFDTQSOYVGLAALENEOQOIDTRAALVEKRLRYLMGTGRNTBEEAMM 961

Db 874 MIEDR--OKEKSYSHOTVQL--VIEKEQALADINS--VEKS--LADIFERRYKEVL 924  
 Qy 962 QEWFMVNKNALLRMNO--LSLKEHDLERRVELL-----NRELRM--LA 1006  
 Db 925 EGP---RKNEBEVLRCAQBYLSRVK--EORYQALKVAEEKLDRANAETAQVRGKA 977  
 Qy 1007 IEWQKTEAQKRBCOLLDLBELVALVNKRULVRDQAOKQARSEDEHLERTLSNGKM 1066  
 Db 978 QEQQAHQASLRKEQ----RVDALERTLEQNKIEB---LTKICDELIAM 1023  
 Qy 1067 AK 1068  
 Db 1024 GK 1025

RESULT 11  
 US-09-949-016-10870  
 ; Sequence 10870, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CLO01307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastaSBQ for Windows Version 4.0  
 ; SEQ ID NO 10870  
 ; LENGTH: 1034  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-949-016-10870

Query Match 5.2%; Score 285; DB 2; Length 1034;  
 Best Local Similarity 21.2%; Pred. No. 2.7e-10; Matches 242; Conservative 153; Mismatches 363; Indels 384; Gaps 58;

Qy 116 DDP--DAEELNPFGDP-----DSERPIETATSPRKTEDSFYNSYNPPKEVQTPQYL 165  
 Db 87 DGRSDSVEGSPRPPSHFSQAVFEDBDKBIASSGT-----YNLDFDNIBLVDTQTL 138  
 Qy 166 NP-----FD-----EPRA 173

Db 139 ERDASAKNQBGKVNTRRKSTDSVPIKSTLSRSLSLQASDFQGASSGNPEVALARDA 198

Qy 174 FVNIKSDPPOSTER-KNTRPVDSKYLADSSKTEEBEDESNPYPYERKSTPPPNLY-- 230  
 Db 199 YSTGGSSASSTSLRKTKCRPPSILK-----KOTTKKETTPEVKETOQBPBESLWPS 251

Qy 231 -NPVQELETERRVKKAP-----PVLSPT-----GVLN-----B 261  
 Db 252 GENTLASETKTE-SAKTKEGPSALLEBTLEPAVGPKAACPLDSESABGVUPPASGGRVQ 310

Qy 262 NTVISAGK--DISTSKPSI-PSPVLGKPKPNASQSLNWCKEVTKNYRGVKITNFTSW 317  
 Db 311 NSPPVGKRLPLTAPAEGBTFSDDSGGOEDSPAKGLSV--RLEFDYSBDK---SSW 362

Qy 318 RNLSCFCAILHHRPDLIDYKSINPQDKKENNICKADEFASTGJSLRJEPSPMLATPD 377  
 Db 363 -----DNQQRNPPTKKIGK-----PVAKMPKRPK--MKKTPB 395

Qy 378 KLTUVTMUYQIRAHPSGOBLNVVQIBENSSKSTYKVGMETDNTSVDQKF--YAE LSD 435  
 Db 396 KLD-NTPSPR--SPAEPNPDI--AKGY--TFDID--KMDPMPFPPRSSK 441

Qy 436 LKREPELQOQPISAVDELSDODDVVFVNDVGUGSSEHOTDDHLSPLSTASPCCRTRUSD 495

Db 442 MQESKLPO-----QSYNFEDD--TCDESPDPKTSKTP 474  
 Qy 496 TEPOQS-----QOSSGRTSGSDPGICSMTDSTAQVLIGKRRKLAETBLSLIVSD 549  
 Db 475 SPSKSPASFEPIPASAMEANGVGDGGL--NPKAK-----KKTBLKTDPFRVK--SP 523  
 Qy 550 KKDMSPP-----FICETDEQKL-----OTLQGSNBEKL 582  
 Db 524 KRSPISDPPSODPTPAATPBTIPVISAUVHATDEEKLAUTVQWKTCMTD--LEADQ 579

Qy 583 ENSRSLCECSDPESIJKTSI--SPTRSKLGYSYSRDLAKKXHASLQRTSDPDARTL 641  
 Db 580 DYPQP---SDLSLTFONETKESSPTEBLDYRNSEYEVEMRKGSSLUPQDDAP----- 628

Qy 642 NHADHSSKIVOHRLLSRQEELKERAVALVLLQARRDAALKAGKANTATAPCNCNQLSDQ 701  
 Db 629 -----KKQALYLMFTSDQESPVQSSPVMSR 662  
 Qy 702 QDEERRQLRERA-----RQLTNEARGSVKMSLPSGEMAAKLUKERSKASBENDN 754  
 Db 663 SPEERELVNTAAKQHVPVRGLAPNQESHQBLQPKSSQKELBAMGL-----GTPSEA 715

Qy 755 REIDTNER-PEGFVVGGBELTNLENDL-----DTPEODNSKVLQDILKLUKLEVO 803  
 Db 716 LEITA---PEGSFASADALLSLRLLAHPVSLGQDADYLEPDLABKNPPLFKQKLOBEFA 771  
 Qy 804 PQVANSPSSAAQAVTESSESDOMKMSGTEDRLTERIQLT-----TERFRNP--WVSK- 853  
 Db 772 IMRTEALKIARQALASRSHODATEAAHPTDVSISKALYSRIGTAEVKPGAGLFOQP 831

Qy 854 --DSTVTKTQLOQFS-----QYIENRPREMORSIQEDTEKGNBKAATETORK 901  
 Db 832 DLDLSQIARAKBTTKEREBSVSEWQKYESRREVEMRKIVIAEYK-----TIAQ 881

Qy 902 PSEDEVILNKGPQDTSQYVUGBALLENQKIDTRALVKEKRYLMDTGTNTBEMM 961  
 Db 882 MIEDR--OKEKSYSHOTVQL--VIEKEQALADINS--VEKS--LADIFERRYKEVL 932

Qy 962 QEWFMVNKNALLRMNO--LSLKEHDLERRVELL-----NRELRM--LA 1006  
 Db 933 EGP---RKNEBEVLRCAQBYLSRVK--EORYQALKVAEEKLDRANAETAQVRGKA 985

Qy 1007 IEWQKTEAQKRBCOLLDLBELVALVNKRULVRDQAOKQARSEDEHLERTLSNGKM 1066  
 Db 986 QEQQAHQASLRKEQ----RVDALERTLEQNKIEB---LTKICDELIAM 1031  
 Qy 1067 AK 1068

Db 1032 GK 1033

RESULT 12  
 US-09-210-767-42273  
 ; Sequence 42273, Application US/09210767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hamburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/210,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62317  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 42273  
 ; LENGTH: 153  
 ; TYPE: PRT  
 ; ORGANISM: *Drosophila melanogaster*  
 ; US-09-210-767-42273

Query Match 5.2%; Score 283.5; DB 2; Length 153;  
 Best Local Similarity 53.1%; Pred. No. 2.6e-11; Matches 52; Conservative 18; Mismatches 27; Indels 1; Gaps 1;

RESULT 13  
US-09-664-958-8  
Sequence 8, Application US/09664958  
; Patent No. 6916912  
; GENERAL INFORMATION:  
; APPLICANT: Trakht, Ilya  
; APPLICANT: Canfield, Robert  
; APPLICANT: Rudchenko, Sergei  
; TITLE OF INVENTION: No. 6916912el Tumor-Associated Marker  
; FILE REFERENCE: 057560240  
; CURRENT APPLICATION NUMBER: US/09/664, 958  
; CURRENT FILING DATE: 2000-09-18  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 912  
; TYPE: PRT  
; ORGANISM: Human  
US-09-664-958-8

Query Match : 5.0%; Score 276.5; DB 2; Length 912;  
Best Local Similarity 22.0%; Pred. No. 8.4e-10;  
Matches 159; Conservative 103; Mismatches 270; Indels 191; Gaps 33;

QY 289 NASQSLILWCKEVTKNYRGKTTINFTSWRNGLFLSCAIIHHRPDLIDYKSLNPODIKEN 348  
Db 163 SAKEGILLWCKRKTPAKYKNVNQFHISWKGLAFNALIHRHPDLIEDKLKRDOPVTN 222  
Qy 349 NKKAVD-GFASIGIRPLPSDMVLAIPDKLTWMTYQIRAHSGQELNVQIEENSS 407  
Db 223 LNAFAFEVKYLDIPKMDAEDIVNTARPFDEKAIMTYVSSFYHAQKETEPANRI 282  
Qy 408 KSTYKGVNEYDTNSVDOQKFYABSLKRE-----PELOQPIGAVDFL 453  
Db 283 CKVLAV-NOEBCSTSMDYEKLGASDILLEWIRTTFWPLEDRVPQKIQEMQKLEFRDY- 340  
Qy 454 SODPSVFVNNSGVGSESEKTPDHLSPETASTPACYCRTSDETEOKSOQSGRSGRSGDD 513  
Db 341 -----RRVH---KDPKVOK-----352  
Qy 514 PGICS--NDSTOQVLGKK--RLKAEIILSLSJ---YVSDKKDKMSPPFICEED 564  
Db 353 --COLBINFNTSVQTLRNPAFMPSECKNSDINNGWQHLQPKGVEEWLINEIRR 409  
Qy 565 BQKLOTLIGNSLEKEKLENSSL-BCRSPDESPPIKTSLSPTSKLGYSYSDIDLAKKK 623  
Db 410 LERLUDL-----AEKFRQKASIRHAWTQKEMALKHRYETATL---D-KALIRK 457  
Qy 624 HASLRQTESPDADRTTLNHDHSKTKVORHLSRQEELGERARYTLEBRRDAALKAGN 683  
Db 458 HEAP---ESD-----LAHQDREQ---TAASQELNE-----LDDYD 489  
Qy 684 KHNTWATPPCNRQLSQDQQ----BERRQRLRERAROLIAARSGVMSLPSYGM 736  
Db 490 SHNVTTR---C-QKICDQWMLALGSLTHSRRLRAELEKTEKOL-----LDDQHLYAKP 539  
Qy 737 AAEKUKERSKASGDENDNIDTNEBRIPEGTVGGDELNLENDLT----PEONS 789  
Db 540 AAPNNMMBESAMEDIQDMPTVHTIBI-EG-LISAHQDFKSTLPADRERAILHPOGQ 597  
Qy 790 KLVLDLKLU-----LEVOPQVANSPSSAAQAV-----TSSBODMKSGREDLT 835

RESULT 14  
US-09-664-958-10  
; Sequence 10, Application US/09664958  
; Patent No. 6916912  
; GENERAL INFORMATION:  
; APPLICANT: Trakht, Ilya  
; APPLICANT: Canfield, Robert  
; APPLICANT: Kalantarov, Gary  
; APPLICANT: Rudchenko, Sergei  
; TITLE OF INVENTION: No. 6916912el Tumor-Associated Marker  
; FILE REFERENCE: 057560240  
; CURRENT FILING DATE: 2000-09-18  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 883  
; TYPE: PRT  
; ORGANISM: Human  
US-09-664-958-10

Query Match : 5.0%; Score 274; DB 2; Length 883;  
Best Local Similarity 21.6%; Pred. No. 1.2e-09;  
Matches 166; Conservative 111; Mismatches 298; Indels 194; Gaps 34;

Qy 289 NASQSLILWCKEVTKNYRGKTTINFTSWRNGLFLSCAIIHHRPDLIDYKSLNPODIKEN 348  
Db 137 SAKEGILLWCKRKTPAKYKNVNQFHISWKGLAFNALIHRHPDLIEDKLKRDOPVTN 196  
Qy 349 NKKAVD-GFASIGIRPLPSDMVLAIPDKLTWMTYQIRAHSGQELNVQIEENSS 407  
Db 197 LNAFAFEVKYLDIPKMDAEDIVNTARPFDEKAIMTYVSSFYHAQSG---AOKAETAA 251  
Qy 408 KSTYKGVNEYDTNSVDOQKFYABSLKRE-----PELOQPIGAVDFLQDSVFDVG 467  
Db 252 NRICKV-----LATN-----261  
Qy 468 ESESHQTPDHLSPSTASPACYRTT---KSDTEOKS-QOSGRSGDD-----PGI 516  
Db 262 -QENEHLMEDYEKLGASDILLEWIRRTIPWLEDRVFOKTIQEMQKLEFDYRVRHKPKV 320  
Qy 517 ---CS---NDSTOQVLGKK--RLKAEIILSLSJ---YVSDKKDKMSPPFICEED 564  
Db 321 QBKCOLBINFNTLQPKLRLSNPAFMPSECKNSDINNGWQHLQPKGVEEWLINEIRR 380  
Qy 565 BQKLOTLIGNSLEKEKLENSSL-BCRSPDESPPIKTSLSPTSKLGYSYSDIDLAKKK 624  
Db 381 LERLUDL-----AEKFRQKASIRHAWTQKEMALKHRYETATL---D-KALIRK 428  
Qy 625 ASLRQTESPDADRTTLNHDHSKTKVORHLSRQEELGERARYTLEBRRDAALKAGN 684  
Db 429 EAP---ESD-----LAHQDREQ---TAASQELNE-----LDDYD 460  
Qy 685 HNTWATPPCNRQLSQDQQ----BERRQRLRERAROLIAARSGVMSLPSYGM 738  
Db 461 HNVNTR---C-QKICDQWMLALGSLTHSRRLRAELEKTEKOL---EADOLHL---BYAKRJA 510  
Qy 739 EKLKERSKASGDENDNIDTNEBRIPEGTVGGDELNLENDLTPEONSKVLDLK 798

RESULT 15  
 US-09-091-501B-8  
 ; Sequence 8, Application US/09091501B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Timley, Jonathon M  
 ; TITLE OF INVENTION: utrophin gene expression  
 ; CURRENT APPLICATION NUMBER: US/09/091,501B  
 ; CURRENT FILING DATE: 1998-05-18  
 ; PRIOR APPLICATION NUMBER: PCT/GB96/03156  
 ; PRIOR FILING DATE: 1996-12-19  
 ; PRIOR APPLICATION NUMBER: GB 9525662.8  
 ; PRIOR FILING DATE: 1995-12-19  
 ; PRIOR APPLICATION NUMBER: GB 9615797.9  
 ; PRIOR FILING DATE: 1996-07-25  
 ; PRIOR APPLICATION NUMBER: GB 9622174.2  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 8  
 ; LENGTH: 2008  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (239) .. (250)  
 ; OTHER INFORMATION: Description of Artificial Sequence: Chimeric; Xaa = Unknown  
 US-09-091-501B-8

Query Match 4.9%; Score 270.5; DB 2; length 2008;  
 Best Local Similarity 20.6%; Pred. No. 6.1e-09; Mismatches 349; Indels 301; Gaps 53;  
 Matches 211; Conservative 164; Mismatches 349; Indels 301; Gaps 53;

QY 286 RKKENASOLVWCKEVTKYRGKIKNTFTSMRNLSCAIIHFRPDLIDYKSLNFDI 345  
 Db 148 QDTNEKILLSWTRQTTRPYSQVNVLNFITSWTDGLATNVAUHRHKPDLFSMDRVNMP 207  
 QY 346 KENNKKAYD-GFASIGISRLLERSDMV-----LIAIPDKUT-----VM 382  
 Db 208 IERLEHAFSKAHTYLGEKULDPDVAVHLPLXXXXXXXXXXVEVLRQQVITDAIREVE 267  
 QY 383 TIVYQIRAHPSOBILN----VQRENSSKSTKVGNSETDTWSSVDOQKPYBLSDIKRE 439  
 Db 268 TPKVKKCECEBEBIHQSAVLAEGGSP----RAETTSIVTEVDMDDLSYQIALE 319  
 QY 440 PELOQQPISGAVDLSQDD-----SVFNDMSGVR----- 468  
 Db 320 EULTWLISAEDTFEODDISDVTEBEVKOFOFATHETFMELTAMOSVGSVLAGNQMLTQ 379  
 QY 469 --SESENQTPDDHLSPLSTASPVCRRKS----DTEPOQKQSSG----- 506

Db 380 GTUSBEERFBIQBMQMLNARWEALRVESMEROSRLHDALMELQKQIQLQSSWLTER 439  
 QY 507 RTSGSDDPGICCSMDSTCQAQVLGKRM--LKAEKTLDSL-----Y 546  
 Db 440 RICKMESPIGLDPLPSLQ-KLQBHKSLQNDLDEAQVKVNSLTHMVVTVDENGESATL 498  
 QY 837 -----RLQKTTFRNPPVFSKOSTVAKTQLOQSFQY---IENRPEM---KROSI 881  
 Db 629 QANVUGPMQIQTMKMEI-GRISIERANGTL-EDQJSHLKQYERSIVDYKPNFLDIEQHOLI 686  
 QY 882 QB----DTKKGN-----BEKAALTETORKPSDEBVLNGKFQDSQYVGCALALE 927  
 Db 687 QEAJLFDNQHTNYMEHIVRGWEOLTTARTINEVENOILTRDAKGISOBQWFRASF 746  
 QY 928 NEQKQDITRAALVERKLRYLMDTGRNTERE--ZAMMOBWMLJUNKNA 973  
 Db 747 NHFTDKHSGAGLGRPERKACLISGYDVENDRQGAEFRNIMSLDPNIS 795

QY RESULT 15  
 Db Sequence 8, Application US/09091501B  
 QY ; GENERAL INFORMATION:  
 QY ; APPLICANT: Timley, Jonathon M  
 QY ; TITLE OF INVENTION: utrophin gene expression  
 QY ; CURRENT APPLICATION NUMBER: US/09/091,501B  
 QY ; CURRENT FILING DATE: 1998-05-18  
 QY ; PRIOR APPLICATION NUMBER: PCT/GB96/03156  
 QY ; PRIOR FILING DATE: 1996-12-19  
 QY ; PRIOR APPLICATION NUMBER: GB 9525662.8  
 QY ; PRIOR FILING DATE: 1995-12-19  
 QY ; PRIOR APPLICATION NUMBER: GB 9615797.9  
 QY ; PRIOR FILING DATE: 1996-07-25  
 QY ; PRIOR APPLICATION NUMBER: GB 9622174.2  
 QY ; NUMBER OF SEQ ID NOS: 15  
 QY ; SOFTWARE: PatentIn Ver. 2.1  
 QY ; SEQ ID NO: 8  
 QY ; LENGTH: 2008  
 QY ; TYPE: PRT  
 QY ; ORGANISM: Artificial Sequence  
 QY ; FEATURE:  
 QY ; NAME/KEY: misc feature  
 QY ; LOCATION: (239) .. (250)  
 QY ; OTHER INFORMATION: Description of Artificial Sequence: Chimeric; Xaa = Unknown  
 US-09-091-501B-8

Query Match 4.9%; Score 270.5; DB 2; length 2008;  
 Best Local Similarity 20.6%; Pred. No. 6.1e-09; Mismatches 349; Indels 301; Gaps 53;  
 Matches 211; Conservative 164; Mismatches 349; Indels 301; Gaps 53;

QY 286 RKKENASOLVWCKEVTKYRGKIKNTFTSMRNLSCAIIHFRPDLIDYKSLNFDI 345  
 Db 148 QDTNEKILLSWTRQTTRPYSQVNVLNFITSWTDGLATNVAUHRHKPDLFSMDRVNMP 207  
 QY 346 KENNKKAYD-GFASIGISRLLERSDMV-----LIAIPDKUT-----VM 382  
 Db 208 IERLEHAFSKAHTYLGEKULDPDVAVHLPLXXXXXXXXXXVEVLRQQVITDAIREVE 267  
 QY 383 TIVYQIRAHPSOBILN----VQRENSSKSTKVGNSETDTWSSVDOQKPYBLSDIKRE 439  
 Db 268 TPKVKKCECEBEBIHQSAVLAEGGSP----RAETTSIVTEVDMDDLSYQIALE 319  
 QY 440 PELOQQPISGAVDLSQDD-----SVFNDMSGVR----- 468  
 Db 320 EULTWLISAEDTFEODDISDVTEBEVKOFOFATHETFMELTAMOSVGSVLAGNQMLTQ 379  
 QY 469 --SESENQTPDDHLSPLSTASPVCRRKS----DTEPOQKQSSG----- 506

Search completed: May 20, 2006, 17:16:29  
 Job time : 60 Secs

Sequence 611, APP  
Sequence 57, APP  
Sequence 778, APP  
Sequence 731, APP  
Sequence 732, APP  
Sequence 5681, APP  
Sequence 333910,  
Sequence 3331, APP  
Sequence 3332, APP  
Sequence 1586, APP  
Sequence 3330, APP  
Sequence 12420, APP  
Sequence 6509, APP  
Sequence 6510, APP  
Sequence 6374, APP  
Sequence 4806, APP  
Sequence 2093, APP  
Sequence 8538, APP

Sequence 5342, Application US/10450763  
 Publication No. US200501967541

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc  
 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
 FILE REFERENCE: 790CIP3.US  
 CURRENT APPLICATION NUMBER: US/10450763  
 CURRENT FILING DATE: 2003-05-11  
 PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR FILING DATE: 2001-03-30  
 PRIOR APPLICATION NUMBER: 09/540,217  
 PRIOR FILING DATE: 2000-03-31  
 PRIOR APPLICATION NUMBER: 09/649,167  
 PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736  
 SOFTWARE: Custom  
 SEQ ID NO 53242  
 LENGTH: 1023

TYPE: PT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (284)..(284)  
 OTHER INFORMATION: Actinin-type actin-binding domain protein domain identified by Pfam, accession number BL00019D, p-value=4.200e-19, raw OTHER INFORMATION: of 15.33

FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (237)..(342)  
 OTHER INFORMATION: Calponin homology (CH) domain identified by Pfam, accession OTHER INFORMATION: name CH, E-value=2.4e-17, Pfam score of 71.1  
 US-10-450-763-53242

Query Match 94.2%; Score 5173; DB 5; Length 1023;  
 Best Local Similarity 99.7%; Preq. No. 1.4e-270; Matches 1011; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 63 IGLDDFEDNEDDENRVNQERAKAKTTELINKLNFLDEBAEKLATVNSNPFDPPDAE 122  
 Db 10 LANLDDFEDNEDDENRVNQERAKAKTTELINKLNFLDEBAEKLATVNSNPFDPPDAE 69

Qy 123 LNFPGDPDSEPTETASPRKTEFSYNNSYNPKEVQVTPQYINPFDPEBFAVTIKDSSP 182  
 Db 70 LNFPGDPDSEPTETASPRKTEFSYNNSYNPKEVQVTPQYINPFDPEBFAVTIKDSSP 129

Qy 183 QSTKRKRIRPVDMSKLYADSSKTEEBELDSNPFYEKS TPPNNLNPNVQOLETERV 242  
 Db 130 QSTKRKRIRPVDMSKLYADSSKTEEBELDSNPFYEKS TPPNNLNPNVQOLETERV 189

Qy 243 KKKAPAPVPLSPKTGVLENNTSAGKOLSTS PKSPSPSPVSPVLGRKPNAQSLLWCKEVT 302  
 Db 190 KKKAPAPVPLSPKTGVLENNTSAGKOLSTS PKSPSPSPVSPVLGRKPNAQSLLWCKEVT 249

Qy 303 KQYRGVKITNFTSWRNGLSFCALHFRPDLDIYKSNPQDITKENNKAYDGFSAGISGTS 362  
 Db 250 KQYRGVKITNFTSWRNGLSFCALHFRPDLDIYKSNPQDITKENNKAYDGFSAGISGTS 309

Qy 363 RLEPSDMVLAIPDKLTVMTTLYQIRAHFSQBLNVVOIRENSSKSTYKVGYETDTS 422  
 Db 310 RLEPSDMVLAIPDKLTVMTTLYQIRAHFSQBLNVVOIRENSSKSTYKVGYETDTS 369

Qy 423 SDQEKYAEELSLKREPELQPIGAVDPLSQDDSVFUNDSCVGESSEHQPDDHSP 482  
 Db 370 SDQEKYAEELSLKREPELQPIGAVDPLSQDDSVFUNDSCVGESSEHQPDDHSP 429

Qy 483 STASPICRTKSDTEPOKSQSSGRGTSDDPGICNSDTSQAVLIGKRLKJAKETEL 542  
 Db 430 STASPICRTKSDTEPOKSQSSGRGTSDDPGICNSDTSQAVLIGKRLKJAKETEL 489

Qy 901 KPSDEVALKGPKOTSQYVNGELAILENEQOIDPDTAALYKLYLMDTGRNTTTEAM 960  
 Db 901 KPSDEVALKGPKOTSQYVNGELAILENEQOIDPDTAALYKLYLMDTGRNTTTEAM 960

Qy 961 MQEWMLTNNKALLRMMQLSLLKEHDILERRVLLNLRLRAMIAEDQKTEAQKRE 1020  
 Db 961 MQEWMLTNNKALLRMMQLSLLKEHDILERRVLLNLRLRAMIAEDQKTEAQKRE 1020

Qy 1021 QLLIDELVALVNKGDALVRLDQAQKQABEDEHEHLERTLBONKGKMAKEEBCVHQ 1076  
 Db 1021 QLLIDELVALVNKGDALVRLDQAQKQABEDEHEHLERTLBONKGKMAKEEBCVHQ 1076

RESULT 2  
US-10-450-763-53242

QY 603 IUPSTSKLGYSSRJDALLAKKHASIAROTESDPPDARTTLNADHSKIVORHLRSQEEL 662  
 Db 550 IUPTSKLGYSSRJDALLAKKHASIAROTESDPPDARTTLNADHSKIVORHLRSQEEL 609  
 QY 663 KERARYTLEQRDRDAALKAGKHNNTATPCCNRQLSDQDDEERRQRARQJABR 722  
 Db 610 KERARYTLEQRDRDAALKAGKHNNTATPCCNRQLSDQDDEERRQRARQJABR 669  
 QY 723 SGVKNSELPSYGEMAAEKLKERSKASGDDENDNIEIDTNERETPEGFVGGDELNL 782  
 Db 670 SGVKNSELPSYGEMAAEKLKERSKASGDDENDNIEIDTNERIPEGFVGGDELNL 729  
 QY 783 DTPEOKSKVLDLKLKLEYEQPVANSPSAOKAVTESSEQDMGSGTEDRLTBLQKT 842  
 Db 730 DTPEOKSKVLDLKLKLEYEQPVANSPSAOKAVTESSEQDMGSGTEDRLTBLQKT 789  
 QY 843 ERPRPVPVFSKOSTRKTQSQYIENPEMKQRSIODETKGENEKAITETORKP 902  
 Db 790 ERPRPVPVFSKOSTRKTQSQYIENPEMKQRSIODETKGENEKAITETORKP 849  
 QY 903 SEDEVALKGFRDTTSQYVVGELAALENEQKODTRALVERKLRYMDGRNTEREAMMO 962  
 Db 850 SEDEVALKGFRDTTSQYVVGELAALENEQKODTRALVERKLRYMDGRNTEREAMMO 909  
 QY 963 EWFMLVNLNKKNLIRRNQSLIKEHDLERRYELNRELAMATEDWQTEAQKREOL 1022  
 Db 910 EWFMLVNLNKKNLIRRNQSLIKEHDLERRYELNRELAMATEDWQTEAQKREOL 969  
 QY 1023 LLDDELVALVNRDALVRLDQDAQKOBEEDEHLERTLEONGKMAKEECKVLQ 1076  
 Db 970 LLDDELVALVNRDALVRLDQDAQKOBEEDEHLERTLEONGKMAKEECKVLQ 1023

RESULT <sup>3</sup>  
 US-10-408-765A-1942  
 ; Sequence 1942, Application US/10408765A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Faby, Boin D.  
 ; APPLICANT: Zhang, Bing  
 ; APPLICANT: Gibson, Bradford W.  
 ; APPLICANT: Taylor, Steven W.  
 ; APPLICANT: Gleim, Gary M.  
 ; APPLICANT: Watnock, Dale E.  
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
 ; FILE REFERENCE: 660988-465  
 ; CURRENT APPLICATION NUMBER: US/10/408,765A  
 ; CURRENT FILING DATE: 2003-04-04  
 ; NUMBER OF SEQ ID NOS: 3077  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1942  
 ; LENGTH: 882  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-408-765A-1942

Query Match Similarity 81.7%; Score 4485; DB 4; Length 882;  
 Best Local Similarity 100.0%; Pred. No.: 1\_5e-233; Length 882;  
 Matches 882; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 MSKLYADSSKTESEELDSENPPYEPKSTPPNPLVNPYOBLETERRVKRAPPPVSP 254  
 Db 1 MSKLYADSSKTESEELDSENPPYEPKSTPPNPLVNPYOBLETERRVKRAPPPVSP 60  
 QY 255 KTGVLIENTVSAKDLSTSPPKSPSPVLRKNAQSILVWCKEVNTYRGKINTP 314  
 Db 61 KTGVLIENTVSAKDLSTSPPKSPSPVLRKNAQSILVWCKEVNTYRGKINTP 120  
 QY 315 TSWRGLSLRCAILHFRPDIDYSLNPODIKENKKAvgDGFAStGSIISLPSDMVLA 374  
 Db 121 TSWRGLSLRCAILHFRPDIDYSLNPODIKENKKAvgDGFAStGSIISLPSDMVLA 180

RESULT <sup>4</sup>  
 US-10-450-763-53241  
 ; Sequence 53241, Application US/10450763  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HYSEQ, Inc  
 ; TITLE OF INVENTION: NOVEL NUCLEAR ACIDS AND POLYPEPTIDES  
 ; FILE REFERENCE: 790CIP3/US  
 ; CURRENT APPLICATION NUMBER: US/10/450,763  
 ; CURRENT FILING DATE: 2003-01-11  
 ; PRIOR APPLICATION NUMBER: PCT/US1/08631  
 ; PRIOR FILING DATE: 2001-03-30  
 ; PRIOR APPLICATION NUMBER: 09/540,217  
 ; PRIOR FILING DATE: 2000-03-31  
 ; PRIOR APPLICATION NUMBER: 09/1649,167  
 ; PRIOR FILING DATE: 2000-08-23  
 ; NUMBER OF SEQ ID NOS: 60736  
 ; SOFTWARE: Custom  
 ; SEQ ID NO: 53241  
 ; LENGTH: 669  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:

; NAME/KEY: DOMAIN  
; LOCATION: (61)..(91)  
; OTHER INFORMATION: Actinin-type actin-binding domain proteins domain identified  
; OTHER INFORMATION: by eMATRIX, accession number BLO0019D, p-value=4.200e-19, raw score  
; OTHER INFORMATION: of 15.33  
; PRIORITY:  
; NAME/KEY: DOMAIN  
; LOCATION: (42)..(147)  
; OTHER INFORMATION: Calponin homology (CH) domain identified by PFam, accession  
; US-10-450-763-53241  
; OTHER INFORMATION: name CH, E-value=2.4e-17, PFam score of 71.1  
; QUERY Match 57.4%; Score 3151; DB 5; Length 669;  
; Best Local Similarity 89.5%; Pred. No. 1e-161; Mismatches 6; Indels 56; Gaps 4;  
; Matches 634; Conservative 6; Mismatches 12; Indels 56; Gaps 4;  
; Qy 248 APPVILSPKPGVGLNEVTSAGKDLSTS--PKPSPTSPSPVPLGRKRNQASQSLIVWCKEVTKY 305  
; Db 2 AKPVLYKKG-G-NQGVAIPDVAWEAEPSPISPVLGRKRNQASQSLIVWCKEVTKY 365  
; Qy 306 RGVKINTNFTSWRNLGSLPCAILHHRPDLIDYKSNPDKIENKKAYDGFASIGISRL 365  
; Db 60 RGVKINTNFTSWRNLGSLPCAILHHRPDLIDYKSNPDKIENKKAYDGFASIGISRL 119  
; Qy 366 BPSDMVLLAIPDGLTWTMVLQIRAHFSGQELNVQIERNSSGTYKGVNEYDTNSVD 425  
; Db 120 BPSDMVLLAIPDGLTWTMVLQIRAHFSGQELNVQIERNSSGTYKGVNEYDTNSVD 179  
; Qy 426 QEKVYAELSDLKEPELQOPIGSAGWDVSQDSVFVNDGGVGESEBENQTPDDHLSSTA 485  
; Db 180 QEKVYAELSDLKEPELQOPIGSAGWDVSQDSVFVNDGGVGESEBENQTPDDHLSSTA 239  
; Qy 486 SPYCRRTKSDEPDKSODSSGRTSGSDPREGICNTSDAQVLAQVILGKRLLKATLDSL 545  
; Db 240 SPYCRRTKSDEPDKSODSSGRTSGSDPREGICNTSDAQVLAQVILGKRLLKATLDSL 299  
; Qy 546 YVSDKKKOMSPPICEETDEQKLTDIGSNSLKEKLENSLSCRSUPESPIKTLSP 605  
; Db 300 YVSDKKKOMSPPICEETDEQKLTDIGSNSLKEKLENSLSCRSUPESPIKTLSP 359  
; Qy 606 TSCLGYSYSDLDIAKKGHASLQTESPDADRTLNADHSSKIVQHRLLRQBELKER 665  
; Db 360 TSCLGYSYSDLDIAKKGHASLQTESPDADRTLNADHSSKIVQHRLLRQBELKER 405  
; Qy 666 ARVILEBQARRDAALKAKGHNHTNTATPPCNRLSDQDPERRERQRLZEARSGV 725  
; Db 406 -----QDERRRQRLZEARSGV 430  
; RESULT 6  
; US-10-450-763-53239  
; Sequence 39276, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; TITLE OF INVENTION: DIOSPHYLIC GENES.  
; FILE REFERENCE: C1000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1998-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; FILE REFERENCE: 790C1P/US

CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-05-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 53239  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (65)..(97)  
; OTHER INFORMATION: REV Protein (anti-repression transactivator protein) domain  
; OTHER INFORMATION: identified by eMATRIX, accession number PF0042A, p-value=9.521e-  
; OTHER INFORMATION: 09, raw score of 14.34  
; US-10-450-763-53239  
; QUERY Match 19.0%; Score 1045; DB 5; Length 221;  
; Best Local Similarity 84.4%; Pred. No. 1e-48; Mismatches 0; Indels 36; Gaps 1;  
; Matches 217; Conservative 0; Mismatches 4; Indels 36; Gaps 1;  
; Qy 628 ROTESDPADRTLNADHSSKIVQHRLRSOBELKERARVILLEQARDRAALKAGNKNT 687  
; Db 1 RWNSSDPADRTLNADHSSKIVQHRLRSOBELKERARVILLEQARDRAALKAGNKNT 60  
; Qy 748 SGENDDNIEIDTNEEIPGFVVGGDSELTNLENLDTFEONSKLVDJLKLUKEVQQVA 807  
; Db 121 SG-----EQNSKLVDLKLUKEVQQVA 144  
; Qy 808 NSPSSAAKAVTTESSBQDMKSGTEDLRTERLQKTERPRNPVVFQSKOSTVRKIQLOSRQ 867  
; Db 145 NSPSSAAKAVTTESSBQDMKSGTEDLRTERLQKTERPRNPVVFQSKOSTVRKIQLOSRQ 204  
; Qy 888 YIENRPENKRQRSIQED 884  
; Db 205 YIENRPENKRQRSIQED 221

PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: 60/911,637  
PRIOR FILING DATE: 2000-03-23  
NUMBER OF SEQ ID NOS: 43008  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 39276  
LENGTH: 957  
TYPE: PRT  
ORGANISM: DROSOPHILA  
US-11-037-143-39276

Query Match 18.6%: Score 1020.5; DB 6; Length 957;  
Best Local Similarity 27.4%; Pred. No. 1.5e-46;  
Matches 316; Conservative 166; Mismatches 279; Indels 391; Gaps 38;

QY 1 MKQVQASPMPTQDVKLKPPLKVKVMSALQPSLSCIFRECKATDEMDQSLASLVSMKQ 60  
Db 121 MKYKASIBESTSQESTPSLKEVSKITAALELTSCFVRGKATDEMDQSVSMMVAN 180  
QY 61 ADIGNLDDPBR-----DNEDDDENRVRNQ-----BEKAAK 89  
Db 181 NDVARPLDDIADIPDGFSPBTNDNFDFQOLEMTTSINGCIVATPOSVSPLSEDPPIP 240  
QY 90 ITELINKLAKFLDRAEAKDLATVNSNPFDDAEALNPFGUPDS-----EEPI--135  
Db 241 LAEBSNPPLM-----ELDAGKREANKUDLPTAAGCGSSGABESLKTPNGLQHVVNDPTIKS 298  
QY 136 -TEASPRKTE-DSPTNNSYNPFPKEVQTOYLINPDEP-----AFVTIKDSPPOS 184  
Db 299 PEYTKQPKPVESLRSKTEDEQDMVTPBENPKVKPKKRALFPTECED-BGD 357  
QY 185 TKRKNIRPVDMSKYLYADSSTKTEBEDLSSNPFPVBPKSTPPNMLVNPNVQBLER---- 240  
Db 358 LRVESVKE-DTKT-K-GDNSTTKEKPEKPEQSQQSDASSVVPSPAKRPELQPPLNUKKSTEP 415  
QY 241 -RVKRKAPAPPVLSPTKTVLANTENTWSAGKDLSTERPKS---P-PSPVLRKERAQSIL 235  
Db 416 SQTPEASAPV-----ASVINE---SIGCFSTSGSLANSLSKPEVKIVL-KENTPGDILL 465  
QY 296 WCKCEVTKYRGKVKTINFITSWRKGULFCALHHRPDIDYKSLNPQDIKENKKANG 355  
Db 466 BWCKEVTKYOPVNVKVNLTISWRGMACAIHHPVPELJDMISLSAHDWVGRIGEDA 525  
QY 356 PASIGISRLPLPSOMVLLAIPDKLJUVTMAYQIRAHFSQBLNTVQIBENSSEKTYKVN 415  
Db 526 AESLGIPRVIPEPRDMMLTVPDFGLAVMTLHQLAHTFSKQKLIKQIGSTADESSIVGD 585  
QY 415 YETUNNSVYDQEKEYAELDLKREPELQPISGAVDELSQDDSYEVNDSVGGESEHOT 475  
Db 586 YKSD-NLSQNRINFSHKPKSLLHQNSFDRINGS-----N 619  
QY 476 PDDHLSPTSTASPYCRTKSDEPKSQQSSGRTSGDDPGICNSNTDSTAQVLIGKRRLL 535  
Db 620 KSBQLSPTE-----628  
QY 536 KABTELESDOLYVSDKCKOMSPPFICEETDBQKLOFTDGSNLKEKLENRSUBCRSDPE 595  
Db 629 -----KKDV-----KLN-----ILYNSK-----642  
QY 596 SPIKKULSPTSKLUGYSYRDLDAJAKKKHASLQTESDADRTLTNHADHSKLVORHL 655  
Db 643 -ILDKVLSPTK-----DKNINSASQHAN---QSPM 669  
QY 656 LSROBLKLKERARVILQARDAALKAGNKHNINTATPCNRQLSDQO---DEBRRLQARR 713  
Db 669 LSCOPTPPDSE-----DGKSOPEGKST-----IDPOASERKQRQLEQ 714  
QY 714 ARQJTAEARASGGVKVSELPSYGYEMAEEKLUKERSKASGDENDNITIDTNEBEPGEGVUGGD 773  
Db 715 ARRILETR-----VKSGG-----728  
QY 774 BLTMLENDLADTPBONSKLVDLKLKQKLEVOPQVANSPSSAAQAVTTESSEDQMKSGTDL 833

RESULT 7 US-10-450-763-53240  
; Publication No. US10450763  
; General Information:  
; APPLICANT: HYSEQ, INC  
; TITLE OF INVENTION: NOVEL NUCLEARIC ACIDS AND POLYPERTIDES  
; FILE REFERENCE: 79CIP3JUS  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/1649,167  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO: 53240  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (419)..(451)  
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by  
; OTHER INFORMATION: ematrix, accession number Dm01354J, p-value=2.62e-15, raw score 4.00  
; OTHER INFORMATION: 15.12  
US-10-450-763-53240

Query Match 18.0%: Score 989; DB 5; Length 479;  
Best Local Similarity 67.0%; Pred. No. 3.1e-45;  
Matches 209; Conservative 19; Mismatches 50; Indels 34; Gaps 6;

QY 3 QYASP---MPTQDVKL---KFKP-LSKVKVMSALQPSLSCIFRECKATDEMDQSLAS 54  
Db 36 OHSPKURQUTPSLHSGGPKASPAASSEVAVNLLPAIGTCNSLGTKLBSSA- 94  
QY 55 LVSNKQADTGNDLDFEEDNEDD---ENRVNQBEKAAKITELINKLFLDEAKLAV 110  
Db 95 -VTRAPETVNLQNLASSIDEDQDCIKQAMRSAKSASSEELINKLFLDEAKLAV 153  
QY 111 NSNPFDPPDAEALNPFGUPDSRPITEASPRKTEDSYNNSYNPKEVOTSOYNPDE 170  
Db 154 NSNPFDPPDAEALNPFGUPDSRPITEASPRKTEDSYNNSYNPKEVOTSOYNPDE 213  
QY 171 PRAFTIKDPSPOSTKRNIRPVDMSKLYAASSKSTEREELDSENFPVBPKSTPPNMLV 230  
Db 214 PEARFTIKDPSPOSTKRNIRPVDMSKLYAASSKSTEREELDSENFPVBPKSTPPNMLV 273

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QY 231 NPQVQELETERVKRKAPAPPVLSPPKGCVLNLNTVSAGKDLSTSPKCCTHVCUTLPRRHCMCK 333
Db 274 NPVOQLETERVKRKAPAPPVLSPPKGCVLNLNTVSAGKDLSTSPKCCTHVCUTLPRRHCMCK 333
QY 276 -----PSPISP 282
Db 334 HMHTTPATPLP 345

RESULT 8
US-10-472-576-5
; Sequence 5, Application US/10473576
; Publication No. US20040101884A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: LU, DYUNG ANNA M.
; APPLICANT: ARVIZU, CHANDRA S.
; APPLICANT: GANDHI, AMEENA R.
; APPLICANT: HARRIA, APRIL J.A.
; APPLICANT: DING, LI
; APPLICANT: LU, YAN
; APPLICANT: RAMKUMAR, JAYALAXMI
; APPLICANT: SWARNAKAR, ANTTA
; APPLICANT: TANG, Y. TOM
; APPLICANT: YUE, HENRY
; APPLICANT: TRAN, BAO
; APPLICANT: LEE, SOO YUEN
; APPLICANT: WARREN, BRIDGET A.
; APPLICANT: NGUYEN, DANIEL B.
; APPLICANT: THANGAVELU, KAVITHA
; APPLICANT: YAO, MONIQUE G.
; APPLICANT: ELLIOTT, VICKI S.
; APPLICANT: BAUGHN, MARIAH R.
; APPLICANT: EMERLING, BROOKE M.
; APPLICANT: LAL, PREETI G.
; APPLICANT: GIEZEN, KIMBERLY J.
; APPLICANT: BECKER, SHANYA D.
; APPLICANT: MARQUIS, JOSEPH P.
; APPLICANT: KABIR, AMY E.
TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
FILE REFERENCE: PP-0221 USN
CURRENT APPLICATION NUMBER: US/10-472-576
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: PCT/US02/19809
PRIOR FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 60/280, 387
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/282, 335
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/286, 663
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/285, 484
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 60/350, 702
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/351, 749
NUMBER OF SEQ ID NOS: 46
SEQUENCE: PERL Program
SEQ ID NO 5
LENGTH: 1523

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME: KEY: misc feature
OTHER INFORMATION: Incyte ID No: 1510943CD1
US-10-472-576-5

RESULT 9
US-03-864-761-42973
; Sequence 42973, Application US/03864761
; Patent No. US20040873A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 242633.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO: 42978
LENGTH: 175
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
OTHER INFORMATION: MAP TO AC007098.2
OTHER INFORMATION: EXPRESSED IN HHLA, SIGNAL = 0.61
OTHER INFORMATION: SWISSPROT HIT: P32583, EVALUE 1.10e-01
US-10-029-386-33831

Query Match          16.3%; Score 89%; DB 4; Length 175;
Best Local Similarity 100%; Pred. No. 8.1e-41; Mismatches 0; Indels 0; Gaps 0;
Matches 1/5; Conservative
Qy      352 AYDFASIGISRLIEPDSMLLAIPKLTWMTYQIRAHPSGELNVQIERNSSKTY 411
Db      1 AYDFASIGISRLIEPDSMLLAIPKLTWMTYQIRAHPSGELNVQIERNSSKTY 60
Qy      412 KVGNEYDTNSVSDQKFAYABLSDLKRPELQLQPIGAVDPLSODSYFVNDSGVGESES 471
Db      61 KVGNEYDTNSVSDQKFAYABLSDLKRPELQLQPIGAVDPLSODSYFVNDSGVGESES 120
Qy      472 EHQTDDHHSUPSTASPYCARTKSDEPOKSOQSRSRTGSDDPICSNTDQAQ 526
Db      121 EHQTDDHHSUPSTASPYCARTKSDEPOKSOQSRSRTGSDDPICSNTDQAQ 175

ORGANISM: Homo sapiens
FEATURE:
FEATURE:
OTHER INFORMATION: EXPRESSED IN HHLA, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.98
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.76
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
OTHER INFORMATION: EST HUMAN HIT: BF307519.1, EVALUE 2.00e-41
OTHER INFORMATION: SWISSPROT HIT: P32583, EVALUE 8.10e-02
US-09-864-761-42978

Query Match          16.3%; Score 89%; DB 3; Length 175;
Best Local Similarity 100.0%; Pred. No. 8.1e-41; Mismatches 0; Indels 0; Gaps 0;
Matches 1/5; Conservative
Qy      352 AYDGASIGISRLIEPDSMLLAIPKLTWMTYQIRAHPSGELNVQIERNSSKTY 411
Db      1 AYDGASIGISRLIEPDSMLLAIPKLTWMTYQIRAHPSGELNVQIERNSSKTY 60
Qy      412 KVGNEYDTNSVSDQKFAYABLSDLKRPELQLQPIGAVDPLSODSYFVNDSGVGESES 471
Db      61 KVGNEYDTNSVSDQKFAYABLSDLKRPELQLQPIGAVDPLSODSYFVNDSGVGESES 120
Qy      472 EHQTDDHHSUPSTASPYCARTKSDEPOKSOQSRSRTGSDDPICSNTDQAQ 526
Db      121 EHQTDDHHSUPSTASPYCARTKSDEPOKSOQSRSRTGSDDPICSNTDQAQ 175

RESULT 11
US-11-097-143-23565
; Sequence 23565, Application US/11097143
; Publication No. US20050208558A1
GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEAR ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO: 33831
LENGTH: 175
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
OTHER INFORMATION: MAP TO AC007098.2
OTHER INFORMATION: EXPRESSED IN HHLA, SIGNAL = 0.61
OTHER INFORMATION: SWISSPROT HIT: P32583, EVALUE 1.10e-01
US-10-029-386-33831

Query Match          16.3%; Score 89%; DB 4; Length 175;
Best Local Similarity 100%; Pred. No. 8.1e-41; Mismatches 0; Indels 0; Gaps 0;
Matches 1/5; Conservative
Qy      352 AYDFASIGISRLIEPDSMLLAIPKLTWMTYQIRAHPSGELNVQIERNSSKTY 411
Db      1 AYDFASIGISRLIEPDSMLLAIPKLTWMTYQIRAHPSGELNVQIERNSSKTY 60
Qy      412 KVGNEYDTNSVSDQKFAYABLSDLKRPELQLQPIGAVDPLSODSYFVNDSGVGESES 471
Db      61 KVGNEYDTNSVSDQKFAYABLSDLKRPELQLQPIGAVDPLSODSYFVNDSGVGESES 120
Qy      472 EHQTDDHHSUPSTASPYCARTKSDEPOKSOQSRSRTGSDDPICSNTDQAQ 526
Db      121 EHQTDDHHSUPSTASPYCARTKSDEPOKSOQSRSRTGSDDPICSNTDQAQ 175

Publication No. US20030194704A1
GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEAR ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO: 33831
LENGTH: 175
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
OTHER INFORMATION: MAP TO AC007098.2
OTHER INFORMATION: EXPRESSED IN HHLA, SIGNAL = 0.61
OTHER INFORMATION: SWISSPROT HIT: P32583, EVALUE 1.10e-01
US-10-029-386-33831

Query Match          16.3%; Score 89%; DB 4; Length 175;
Best Local Similarity 100%; Pred. No. 8.1e-41; Mismatches 0; Indels 0; Gaps 0;
Matches 1/5; Conservative
Qy      352 AYDFASIGISRLIEPDSMLLAIPKLTWMTYQIRAHPSGELNVQIERNSSKTY 411
Db      1 AYDFASIGISRLIEPDSMLLAIPKLTWMTYQIRAHPSGELNVQIERNSSKTY 60
Qy      412 KVGNEYDTNSVSDQKFAYABLSDLKRPELQLQPIGAVDPLSODSYFVNDSGVGESES 471
Db      61 KVGNEYDTNSVSDQKFAYABLSDLKRPELQLQPIGAVDPLSODSYFVNDSGVGESES 120
Qy      472 EHQTDDHHSUPSTASPYCARTKSDEPOKSOQSRSRTGSDDPICSNTDQAQ 526
Db      121 EHQTDDHHSUPSTASPYCARTKSDEPOKSOQSRSRTGSDDPICSNTDQAQ 175

Publication No. US20030194704A1
GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEAR ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO: 33831
LENGTH: 175
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
OTHER INFORMATION: MAP TO AC007098.2
OTHER INFORMATION: EXPRESSED IN HHLA, SIGNAL = 0.61
OTHER INFORMATION: SWISSPROT HIT: P32583, EVALUE 1.10e-01
US-10-029-386-33831

Query Match          16.3%; Score 89%; DB 4; Length 175;
Best Local Similarity 100%; Pred. No. 8.1e-41; Mismatches 0; Indels 0; Gaps 0;
Matches 1/5; Conservative
Qy      352 AYDFASIGISRLIEPDSMLLAIPKLTWMTYQIRAHPSGELNVQIERNSSKTY 411
Db      1 AYDFASIGISRLIEPDSMLLAIPKLTWMTYQIRAHPSGELNVQIERNSSKTY 60
Qy      412 KVGNEYDTNSVSDQKFAYABLSDLKRPELQLQPIGAVDPLSODSYFVNDSGVGESES 471
Db      61 KVGNEYDTNSVSDQKFAYABLSDLKRPELQLQPIGAVDPLSODSYFVNDSGVGESES 120
Qy      472 EHQTDDHHSUPSTASPYCARTKSDEPOKSOQSRSRTGSDDPICSNTDQAQ 526
Db      121 EHQTDDHHSUPSTASPYCARTKSDEPOKSOQSRSRTGSDDPICSNTDQAQ 175

```

; ORGANISM: DROSOPHILA  
US-11-097-143-23565

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RESULT 12
US-10-359-012-18
; Sequence 18, Application US/10359012
; Publication No. US20030232419A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: KOLODKIN, Alex L.
; APPLICANT: TEIMAN, Jon R.
; APPLICANT: MAO, Tianyi
; APPLICANT: PAUERKAMP, Ronald J.
; APPLICANT: YU, Hung-Hsiang
; TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPYRIMIDYLIC ACIDS AND METHODS OF USING THE SAME
; TITLE OF INVENTION: AND METHODS OF USING THE SAME
; FILE REFERENCE: JHU1840-3
; CURRENT APPLICATION NUMBER: US/10/359,012
; CURRENT FILING DATE: 2003-02-04
; PRIORITY APPLICATION NUMBER: US 60/388,325
; PRIORITY FILING DATE: 2002-06-13
; PRIORITY APPLICATION NUMBER: US 60/384,302
; PRIORITY FILING DATE: 2002-05-30
; PRIORITY APPLICATION NUMBER: US 60/354,178
; PRIORITY FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1010
; TYPE: PRT
; ORGANISM: Drosophila
; US-10-359-012-18

Query Match          9.2%; Score 507.5; DB 4; Length 1010;
Best Local Similarity    22.1%; Pred. No. 7.6e-19; Matches 228; Conservative 157; Mi matches 319; Indels 329; Gaps 40;
Matches 228; Conservative 157; Mi matches 319; Indels 329; Gaps 40;

QY      291 SQSILVWCKEVTKVTRGKVITNFTTSWRNGLSFCMILHHRPDLIDYKSLNPQDIKENNK 350
QY      13 TKALELYWCRVTVQSYGVKVNEMTTSWRNGLAFCAIHHRPDLIDPDRKLADDIVENND 72
QY      351 KAYTGFAAS-IGISHLLEPSDMVLLAIPDKLTUMTYQIAHFSQELNVVQIEENSSKS 409
QY      73 LAFFTAEKYLGIPALIADAADMVSYEVDRDLSILTSQF----- 111
Db      410 TYKVGNYEFTDNSSVQKEPYAELSDIKREPELQPIGAVDPLSQDD----SVFVND 463
Db      112 -YKV-----LGKSKLKHPRKEEPERLGE--ESEPKPKUMHTVGMPRRDKCQKCNLPVFLAB 161
Db      464 SGVCESESEHQ-----TPDDHSPSTASPYCRRTKSDTATPQ-KSQQSGETSG 510
Db      73 LAFFTAEKYLGIPALIADAADMVSYEVDRDLSILTSQF----- 111
Db      162 RVLVKGKRAYHRTCLKCARCSSLTPGSFTEVNNIYCCTCPDSESEPESDILKLTIT 221
Db      511 SDDPG---ICSNNTSTOQAVLUGKRKLQETLULSDLVSKDKDMSPPFICSETDEO 566
Db      222 TDSPNDKOMVAQGSSDYEAD-----KQBDIDNDIRTDKPNFQPP---SNKDEO 270
Db      567 -XLTQTLIGNSLMEKLU-----ENRSLECSDPESPIK-----KTSLSP---- 605
Db      271 NNBLTINTPVNPILSEERKSFIPLEDEBEGLIEONKSTTPVKPAPEKPKVSTPLDDB 330
QY      606 -----TSKLIGSYSRSDIDLAKKCHASLRQTESTPDADRTLN--HADHSKIVORLL 656
Db      331 QHAGVEQNNDLANSPENDPKEKLUKISSVIYED--DRLVVDIAHPDN-----L 378
QY      657 SROBLERKERRARVILLEQARR-----DAALK-----AGNKINTNTATPPFCNRO--- 697
Db      379 DKOBALNNNTSDALLPFESORAPIPENTQVAIKPENHISPRKRNKFNSNTS--CSIQBGV 436

```



; APPLICANT: YU, Hung-Hsing  
 ; TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPTIDE  
 ; FILE REFERENCE: JHUI840-3  
 ; CURRENT APPLICATION NUMBER: US/10/359,012  
 ; PRIORITY FILING DATE: 2003-02-04  
 ; PRIORITY APPLICATION NUMBER: US 60/388,325  
 ; PRIORITY FILING DATE: 2002-06-13  
 ; PRIORITY APPLICATION NUMBER: US 60/384,302  
 ; PRIORITY APPLICATION NUMBER: US 60/354,178  
 ; PRIORITY FILING DATE: 2002-02-04  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 14  
 ; LENGTH: 863  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-359-012-14

Query Match 9.1%; Score 498.5; DB 4; Length 863;  
 Best Local Similarity 24.9%; Pred. No. 1.9e-18;  
 Matches 218; Conservative 137; Mismatches 367; Indels 153; Gaps 30;

Qy 293 SLIYWCKEVTKNTGRGKUTNFTTSWRNGSFCATLHHRPDLIDYKSINPQDIEKKKA 352  
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 7 ALLAWCRROCEGYRGVERTDLSSSPRDGLAPCATLHHRPDLIDPDSLKDNYFENNLRA 66

Qy 353 YD-GFASIGISRLLEPDMDVLLAIPDKLTVMYLQIRAHSG----- 394  
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 67 FEVAEKELGIPALIDPNDMVSVPDCLSIMTVSQYTNHFCSPGAGVSPRKGLAPCS 126

Qy 395 -----QELNVQTEBENSSTKYKVNEYDTDNSS----- 394  
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 127 PPSVAVPTPEPDVAQGELSSLSQEQTGTPSSTCACQOHVHLVQRYLADGRYHR 186

Db 432 ESDLKREPELQDPIGAVDFFSODDSVFNDSGVGESESERHQTDPDHLSPSTASPVCRR 491  
 187 HCFRCRCCSSTLIP--GAYE-NPREGTIVC-----AEHCA---RLGIGTRSG--TR 230

Qy 492 TKESTEPOKSQOSGRGTSDDPGICSMTDSTAQVLIGKGRULKAAFLTELDLYSDDK 551  
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 291 QBLASPPAGRPTPAPRKASESTTPAPPTPRPSSLQOENLVQAGSSLVNGRLHELPV 350

Db 231 PGPFSPQKQHQOOLAKDVFPGGSSAPAGAAEADGPKAPEARPOIPTKPRVGL 290  
 552 KDM-SPPF-----ICETEOKLQTLDIGSNLEKEKL---ENSRSLECRSDPESPIK 599  
 :|||:|||:|||:|||:|||:|||:|||:|||:  
 351 KURGTPKPSEGTPAPRKOPDPWMTLVQAFPKKCPAPLPPSSPPSDSROVENGG-TEE 409

Qy 600 KTSLSPLSKLGSYSRD---LDA---KCKHASLROTES--DPAADRTLNHADHSK 649  
 650 IWP-----HRLSROELKERARVILLEQARRDAALKAGNKNT-NATPCNRQ 697  
 :|||:|||:|||:|||:|||:  
 410 VAQSPSTASLESKPNYPFEEREDKEEPAAPSLATSPAL--GHPSTPKLHPWGIT 467

Db 698 LSDQDDEERRQLRERARQLIAEARSGKWMSEPSYGEAMAELKERSKASDENDNIEI 757  
 :|||:|||:|||:|||:|||:  
 468 PRSSPKTKRPPRAPSASPLAHASLHSPPSAPSPALSVESLSSBSASQAGEL 527

Qy 758 DTNBETEGFPVUGGDELNLNDLDPBONSLVUDKLUKLL-----VORQANSPSS 812  
 528 LEPPAVEK-----SSSPAVHAAGTPGPMPVSLNSTNSLASSGELVBRVEQMQA 577

Qy 813 A---AQKAVTEASEQDPMKSGTSRDLTERLQKTERFAMPVVISKDSTVRKQLOQSFSQYI 869  
 :|||:|||:|||:|||:|||:  
 578 SGLAPRTRGSSGQPQPKC5AATPTPLWD---RSPVRSPGSS---POLQVNSCK 631

Db 870 ENRPMEMKQRSIQBDTQKGNEERKAATETOREKPSDEDVLNKFK-----DTSQYVV-- 920  
 632 EPFNPKRSPSPATKATKS-----KPVPPAPGHCFLPLIKKVQDQYIPEED 683

Qy 921 --GELAALNEOKQIDTRAALVEKRLYLMDFGRNTBEEAMMQEWMLVNKNALRR 978

RESULT 15  
 US-11-169-011-167  
 ; Sequence 167, Application US/11169041  
 ; Publication No. US200600192841  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER  
 ; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER  
 ; TITLE OF INVENTION: CELLS  
 ; FILE REFERENCE: 10001 NP  
 ; CURRENT FILING DATE: 2005-06-28  
 ; PRIORITY APPLICATION NUMBER: 60/584,405  
 ; NUMBER OF SEQ ID NOS: 527  
 ; SOFTWARE: Patentin version 3.2  
 ; SEQ ID NO 167  
 ; LENGTH: 863  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-169-011-167

Query Match 9.1%; Score 498.5; DB 6; Length 863;  
 Best Local Similarity 24.9%; Pred. No. 1.9e-18;  
 Matches 218; Conservative 137; Mismatches 367; Indels 153; Gaps 30;

Qy 293 SLIYWCKEVTKNTGRGKUTNFTTSWRNGSFCATLHHRPDLIDYKSINPQDIEKKKA 352  
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 7 ALLAWCRROCEGYRGVERTDLSSSPRDGLAPCATLHHRPDLIDPDSLKDNYFENNLRA 66

Qy 353 YD-GFASIGISRLLEPDMDVLLAIPDKLTVMYLQIRAHSG----- 394  
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 67 FEVAEKELGIPALIDPNDMVSVPDCLSIMTVSQYTNHFCSPGAGVSPRKGLAPCS 126

Qy 395 -----QELNVQTEBENSSTKYKVNEYDTDNSS----- 394  
 :|||:|||:|||:|||:|||:|||:|||:  
 127 PPSVAVPTPEPDVAQGELSSLSQEQTGTPSSTCACQOHVHLVQRYLADGRYHR 186

Db 432 ESDLKREPELQDPIGAVDFFSODDSVFNDSGVGESESERHQTDPDHLSPSTASPVCRR 491  
 187 HCFRCRCCSSTLIP--GAYE-NPREGTIVC-----AEHCA---RLGIGTRSG--TR 230

Qy 492 TKESTEPOKSQOSGRGTSDDPGICSMTDSTAQVLIGKGRULKAAFLTELDLYSDDK 551  
 :|||:|||:|||:|||:|||:|||:|||:|||:  
 291 QBLASPPAGRPTPAPRKASESTTPAPPTPRPSSLQOENLVQAGSSLVNGRLHELPV 350

Db 231 PGPFSPQKQHQOOLAKDVFPGGSSAPAGAAEADGPKAPEARPOIPTKPRVGL 290  
 552 KDM-SPPF-----ICETEOKLQTLDIGSNLEKEKL---ENSRSLECRSDPESPIK 599  
 :|||:|||:|||:|||:|||:  
 351 KURGTPKPSEGTPAPRKOPDPWMTLVQAFPKKCPAPLPPSSPPSDSROVENGG-TEE 409

Qy 600 KTSLSPLSKLGSYSRD---LDA---KCKHASLROTES--DPAADRTLNHADHSK 649  
 650 IVP-----HRLSROELKERARVILLEQARRDAALKAGNKNT-NATPCNRQ 697  
 :|||:|||:|||:  
 410 VAQSPSTASLESKPNYPFEEREDKEEPAAPSLATSPAL--GHPSTPKLHPWGIT 467

Db 698 LSDQDDEERRQLRERARQLIAEARSGKWMSEPSYGEAMAELKERSKASDENDNIEI 757  
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 291 QBLASPPAGRPTPAPRKASESTTPAPPTPRPSSLQOENLVQAGSSLVNGRLHELPV 350

Qy 600 KTSLSPLSKLGSYSRD---LDA---KCKHASLROTES--DPAADRTLNHADHSK 649  
 650 IVP-----HRLSROELKERARVILLEQARRDAALKAGNKNT-NATPCNRQ 697  
 :|||:  
 410 VAQSPSTASLESKPNYPFEEREDKEEPAAPSLATSPAL--GHPSTPKLHPWGIT 467

Qy 698 LSDQDDEERRQLRERARQLIAEARSGKWMSEPSYGEAMAELKERSKASDENDNIEI 757

Db 468 PTSSPKTKRPPAPRAPSASPLAHLAHLSHSSEPPSATPSPLSVSLSSESASQAGEL 527  
 Qy 758 DTNERIPEGFVGGGDELNLDTPEKOSKLUDLKLRL---VQPQVANSPPS 812  
 Db 528 IEPPIAVPK-----SSSEPAVHAPGTGPNPVSLSTNSLASSGELVEPRVBQMPQA 577  
 Qy 813 A--AOKAVTTESSEDOMKGSGTEDIKTERLQXITERRNPVFSKOSTVRKTQLOQSFSQYI 869  
 :  
 Db 578 SPGLAPRTRGSSGPQAKPESGATPPLWGD---RSVPSPGSS---PQLOQTKSSCK 631  
 Qy 870 ENRPEMKRORSIQEDTKKGHEKAATTEOPKSSEDEVLNKGPK-----DTSQXWV--- 920  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 632 ENPFNRKPSPPASPARTKKATGCS-----KPVRPPAPGKGGPLIKRKVQADQIPEED 683  
 Qy 921 --GBLALENENQKQIDTRAALVEKURYLMTGRWTEKEERAMMOWEMFLNKKNALIRM 978  
 | | :  
 Db 684 IHGEMDTIERDLDALEHRGVILLEBKURGGINGR---EDOMLVUDWPKLIEHKHULLVRIE 739  
 Qy 979 NQSLSLKEKENDLERRYELLURBLRML---AEDWQKTEAQKREQOLLDIBVALVNRDA 1036  
 :  
 Db 740 SELITYVKOONLEQROADVESELRCILNKPEKDW---TEBDBAREKVLMQSLVTLIEQRNA 797  
 Qy 1037 IVDIDAQEKOAEEDBEHLESTLEQNGKOMKEE 1071  
 | :  
 Db 798 LINCLDBDRORREEEDKMLR-----AMIKKCB 824

Search completed: May 20, 2006, 17:30:18  
 Job time : 193 secs

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GenCore version 5.1.8  
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## OM protein - protein search, using sw model

Run on:

May 20, 2006, 17:27:13 ; Search time 11 Seconds

(Without alignments)

208.951 Million cell updates/sec

**Title:** US-09-856-723a-8  
**Perfect score:** 5489  
**Sequence:** 1 MKQYASPPMPTQTDVKLKFKP..... RTLEQNKGKMKRKEKRCVVLQ 1076

**Scoring table:** BLOSUM62  
Gapop 10.0 , Gapext 0.5

**Searched:** 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

**Database :** Published Applications AA New:  
1: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpaas/US010\_NEW\_PUB.PEP:\*

2: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpaas/US06\_NEW\_PUB.PEP:\*

3: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpaas/US07\_NEW\_PUB.PEP:\*

4: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpaas/US08\_NEW\_PUB.PEP:\*

5: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpaas/PCT\_NEW\_PUB.PEP:\*

6: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpaas/US10\_NEW\_PUB.PEP:\*

7: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpaas/US11\_NEW\_PUB.PEP:\*

8: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpaas/US60\_NEW\_PUB.PEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	255.5	4.7	849	6 US-10-972-140-1
2	233	4.2	871	6 US-10-505-928-100
3	223.5	4.1	3113	6 US-10-505-928-325
4	222.5	4.1	915	6 US-10-523-014-4
5	213.5	3.9	919	7 US-11-251-465-31
6	203	3.7	2829	6 US-10-525-621-1
7	185	3.4	3256	6 US-10-505-928-357
8	184	3.4	1120	6 US-10-505-928-213
9	182	3.3	1384	6 US-10-505-928-799
10	180	3.3	1674	6 US-10-511-937-2587
11	167	3.0	4373	7 US-11-118-524-2
12	166	3.0	851	6 US-10-511-937-2597
13	164.5	3.0	671	6 US-10-196-749-346
14	164	3.0	1610	7 US-11-252-276-22
15	162.5	3.0	186	6 US-10-511-937-2566
16	162	3.0	1125	7 US-11-252-276-152
17	159.5	2.9	1234	7 US-11-327-900-6
18	157	2.9	638	6 US-10-511-937-2610
19	154.5	2.8	1531	6 US-10-505-928-217
20	151	2.8	769	6 US-10-522-043-9
21	150.5	2.7	730	6 US-10-505-928-841
22	150	2.7	798	6 US-10-511-937-2451
23	147.5	2.7	663	7 US-11-169-140-14
24	147.5	2.7	1809	6 US-10-559-415-2
25	147.5	2.7	6	US-10-559-415-2

## ALIGNMENTS

RESULT 1	US-10-972-140-1
;	Sequence 1, Application US/10972140
;	Publication No. US2006008892A1
;	GENERAL INFORMATION:
;	APPLICANT: Wear, Ilona F.
;	APPLICANT: Yang, Shu-Ping
;	APPLICANT: Kimberly-Clark Worldwide, Inc.
;	TITLE OR INVENTION: Detection of Trichomonas
;	FILE REFERENCE: 1441.168051
;	CURRENT FILING DATE: 2004-10-22
;	NUMBER OF SEQ ID NOS: 2
;	SOFTWARE: FASTSEQ for Windows Version 4.0
;	SEQ ID NO 1
;	LENGTH: 849
;	TYPE: PRT
;	ORGANISM: Trichomonas vaginalis
;	US-10-972-140-1
;	Query Match Best Local Similarity 4.7%; Score 255.5; DB 6; Length 849;
;	Matches 170; Conservative 152; Mismatches 285; Indels 219; Gaps 43;
;	Sequence 1, Appli
;	Sequence 100, App
;	Sequence 325, App
;	Sequence 4, Appli
;	Sequence 31, Appli
;	Sequence 1, Appli
;	Sequence 357, App
;	Sequence 213, App
;	Sequence 799, App
;	Sequence 2587, App
;	Sequence 2, Appli
;	Sequence 2597, App
;	Sequence 345, App
;	Sequence 22, Appli
;	Sequence 2556, App
;	Sequence 152, App
;	Sequence 6, Appli
;	Sequence 2610, App
;	Sequence 217, App
;	Sequence 9, Appli
;	Sequence 841, App
;	Sequence 2451, App
;	Sequence 14, Appli
;	Sequence 190, App
;	Sequence 2, Appli

QY 620 AKKGHASLROTESPPADRTTINHADHSKIVORHLLSROELEKARVILLEGARDAL 679  
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;  
 Db 440 VELRINTL-SSQDSVNR-----HISQOLITY-----IKHIEQLNGKLFETNEARI 486  
 QY 680 KAGNKHNTNTATPFCNRLQSDDQE-ERRQRERAROLIAEARSGVKNSLSYGMMA 738  
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;  
 Db 487 --NEYNA-LAQPIYDEIAKPKERVLATSGEJERRTQPLA-----KOAEAPT---KR 532  
 QY 739 EKUKERSKA-SGBENDNBIDTBEEIPCGFVUGGDELNLNLENDLTPEONSKVLKLK 797  
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;  
 Db 533 EHNEIDPFDGLKEUDSHLHLRVNH-----SPTEIRAVYAVTLQH--ITBLN 577  
 QY 798 KILLEVORQVANSISSAAQ---KAVTSESSEQDMKSGTRDLRTERLQTTFRNPVUFS 852  
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;  
 Db 578 KIFB--EMVANFATAPVITDGTALVUTSSH-----IP 609  
 QY 853 KOSTVRKIQOLQSQYIERPMEKRQSTQEDTKGGNIEKAATETORKPSDEVLNKG 912  
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;  
 Db 610 GDAAVKQVE-----ENLASCUDCVR-KDPPPGSQRARSQIQAQL-----I 651  
 QY 913 KOTSOY--VUGELLALENENEOKOIDTRALVELKEURYLMDTGTRIBEEARMQDFWML-- 967  
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;  
 Db 652 KVTVTYSDATGELV-----QARLUDQKQITLAKK-----TFLEEBERKARINNYTVKADE 700  
 QY 968 -VNGKGNALLRMQMSLLEKEDLERVELLNBLRAM-LATEDWQRTBACKGREOLLI 1024  
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;  
 Db 701 HMMTEAHALDGKNSVSD-GRBLEPKOPLY-VREBNNAKEVFEELTBYOLEKDOHJL 758  
 QY 1025 -----DELVALVNLKEDALVALVLDQ---EKQAEBEDHL 1055  
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;  
 Db 759 EITSTPASINIFFENLINH-----DTLVKEIDARIAAANGLEISEBEL 802

**RESULT 2**  
 US-10-505-928-100  
 ; Sequence 100, Application US/10505928  
 ; Publication No. US2006008853241  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ludwig Institute for Cancer Research et al.  
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
 ; FILE REFERENCE: 28967/39178  
 ; CURRENT APPLICATION NUMBER: US/10/505, 928  
 ; CURRENT FILING DATE: 2004-08-27  
 ; PRIOR APPLICATION NUMBER: US 60/363, 019  
 ; PRIOR FILING DATE: 2002-03-07  
 ; SOFTWARE: PatentIn 3.2  
 ; SEQ ID NO: 100  
 ; LENGTH: 2871  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-505-928-100

Query Match 4.2%; Score 233; DB 6; Length 2871;  
 Best Local Similarity 18.4%; Pred. No. 1e-07;  
 Matches 164; Conservative 164; Mismatches 297; Indels 266; Gaps 36;

QY 343 QDICKENNKKAYGFGASIGISRLIEPSMVLALPDKLTUMTYQRAHRSQELNVOI 402  
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;  
 Db 1129 ERFDQQKNDY---QIKAROCCEKENIGWQKLESBEKAKEKEYE-----ERLVNLQ 1179  
 QY 403 EBNSSKSTY----KVGNYETTNSSUQKEFAELSDLK---REPBLQOP----ISGA 449  
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;  
 Db 1180 EBGTRKREBYENLAKVRHYNEMSNL-RNKYETEINITKT-TKEISMOKEDESKNLRNQ 1238  
 QY 450 VPFLS----ODDSVFNDSGYGESESEBHQTPDDHLSPTSPAYCARTKSITPEOKSQ 503  
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;  
 Db 1239 LDRLSRENRLDKEIVRLNDLSIQLATEOR-----RRAEENALOQKA-- 1279  
 QY 504 SSGRTSOSDPDPCSNSTQDQVLUKGKRLKAETLBSIDYVSDIKKDMSPPTCEET 563  
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;  
 Db 1280 ---CSE-----IMOKQHQBIELQVMQRSSEDNARH-----KQS 1312

**RESULT 3**  
 US-10-505-928-325  
 ; Sequence 325, Application US/10505928  
 ; Publication No. US2006008853241  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ludwig Institute for Cancer Research et al.  
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
 ; FILE REFERENCE: 28967/39178  
 ; CURRENT APPLICATION NUMBER: US/10/505, 928  
 ; CURRENT FILING DATE: 2004-08-27  
 ; PRIOR APPLICATION NUMBER: US 60/363, 019  
 ; PRIOR FILING DATE: 2002-03-07  
 ; SOFTWARE: PatentIn 3.2  
 ; SEQ ID NO: 325  
 ; LENGTH: 3113  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-505-928-325

Query Match 4.1%; Score 223.5; DB 6; Length 3113;  
 Best Local Similarity 19.3%; Pred. No. 4.9e-07;  
 Matches 237; Conservative 215; Mismatches 486; Indels 293; Gaps 53;

QY 41 EKGATDDEMSLUSVMSMQADIGN-DDEBEDNE-----DDENVNQEEKA 89  
 Db ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;  
 Db 1572 QCMKMKIQIBOLUSEROBDCIRKQYISBNWQKULTSVTLEMESKLAEBCKT 1631

Qy	Db	90 ITBLINLNPNPDRBAAKDLATNSNPFPDPAA 1632 QLSLBELEVAPLOGQLNLLSSRLGIDTEDA1QGRNEDSIKHEHTSETERTPKDVBHQ	BLNP 125
Qy	Db	126 FGDPDS-----EPITETASPRKTEDSFYNS---YNPPKEVOT-----	161
Qy	Db	1692 ICDKAOQDPLNDIBKITEGALKPTOCBSCGQSPDTNYPGEDTQGSSBCISLFS	1751
Qy	Db	162 -POYLMPPDEPEAPVTKDS-----PPOSTKRKNTRPVMSKLYADSKTTEREELDES	214
Qy	Db	1752 GPNALVPM-----FLANQDINLQJRKVETSNENTRLL---HVIDRDRKVE-----	1797
Qy	Db	215 NPYERKSTPPPNUNPVQSLET----ERRVKRKAAPPULSPKGIVLIENTSAGKD	269
Qy	Db	1798 -----SLANEKEDSKUHLQKVOLMTKIEACTELKTVGELKTR---NSD	1840
Qy	Db	270 LSTSPKPSPISPVLRKPNASQ---SLLWCKEVTNYRGKUTNFTSWR-----	318
Qy	Db	1841 LSKUKYFSCDHQELL-ORVERSEGNSLDEMADKSRREDIGDNVAKUNDWKERTLDVE	1900
Qy	Db	319 NGLS-----FCAILH---HERPDL---IDYSINPOLIKENNTKAVYGFASTGISRLEPS	368
Qy	Db	1901 NELSRTRSEKASIEHAEALYLEADLEVOTEKCLERKENENQK-----	1943
Qy	Db	369 DMVLLAIPDKLTWT-YLIQIRAHFGQEBLNVQLENSSSTYKIGNYEIDTNSSVDQE	427
Qy	Db	1944 --VIVOLEKESLVSUVRBNQNGLNGELTMSKTTALQLSBOMEK--TOELESHQSBLH	1999
Qy	Db	428 KFYAELSDLRBPLRLOOPTISGAVDPLSODDS-----VFVND-----GVGESESEOTPD	477
Qy	Db	2000 CIQVARABVEKSTEL-QTLSSDVSEELKDQHLOEKLQSLRSKOSALSLTCKELEMQIAQ	2059
Qy	Db	478 -----DHLSPSTASPCCRKSDETEPQKSQSSGRSGSDPG---ICNSTDSTAQVL	528
Qy	Db	2060 LINKEKELLVKSESESLOAARLSBSDYE--KLYNTSKALHALVEKGFERALRSTSSEBTHQLR	2117
Qy	Db	529 LGKKR-LKAETLELSDLYVSDKKMSPPTICEETDEQKUQTLDIGSNIURKEJENSRS	587
Qy	Db	2118 RGIKEKURVRIEADEKQHIAKLRKRE---RENDSLK--DVKENJERBLQMEEN	2168
Qy	Db	588 LEC-----RSDPESPIKKTSPLSTSPLKLGYSRSDLACKHASRQTESDDPARDTL	641
Qy	Db	2169 OBLVIIADAENSKAETVLTQIBEMARSLSKVFELDIDVTLASBKENTTKQIORKQGUSL	2228
Qy	Db	642 NHADHSKIVOHRLSQRBEL--KERRAVULQARRDAAKAGN--KHNINTATPPCNR	696
Qy	Db	2229 D-----KLISFKSLBEEKQAOIQUKERSKTAVENTMLQNLKELNTAVALALGD	2277
Qy	Db	697 QLSDQDDE-----ERRQRLRERAKQIABARSGK---MSBTPSYGSEMAEKLKER	744
Qy	Db	2278 OBIMKATEQSLDPPTEEHQJRNSTEKURARLBKKQLCVLUQOLIKE-SEHHADLIKGR	2336
Qy	Db	745 SK-----ASCDENDIEIDNTNEETPEGF-----TUGGGDDELTLN	778
Qy	Db	2337 VENLERBLEIARTNQHQAELAENSGEVEETLAKIGEMTOSLRLGJBLDVTTSRSEKLN	2396
Qy	Db	779 ENDLPBPQNSKLVJLKKKLEVQPVQANSPSSAAQKANTTESSEODMKGT-BDLRTE	836
Qy	Db	2397 TNELQ---KEOPISEBFI-----INSPENTIQEKESEOKVMEKSTAMMILQTO	2445
Qy	Db	837 RLQKTTERFRNPVVFESKDSTRTRKTQJQSFSONYENPEMKQRS1QB-DTRKGN-----	889
Qy	Db	2446 -LKELMERV--AALHNDQBACKAKEQNLSSQVEC-ELEKAQOLLSGLDEAKNNVILQS	2500
Qy	Db	890 -----EKAIAITERKOPSEDEDEVNKGPFDTSOVWGLAALBN-----OKOIDTRA	937
Qy	Db	2501 SVNGLIQEVGQKQKKEKOBEBISRKNOTQDQEO-LVSKLSQVGEHOLWKEQMLBLRN	2559
Qy	Db	938 ALV--EKRLYVLMDFORTNTEREAMMQEWFMVLNUKGAL-IRRMQQLSLRKEHDLERY	994
Qy	Db	2560 LTVELBLOKIQVLOSKNASQDPTLEVQSSVK--NLNBLNLTQMDKMSFVKVNMTAKE	2617
Qy	Db	995 ELLNRERAMI--AEDWQTEAQRKR---EQLL-----DELVALVNRKDVALVRDL	1041

RESULT 4  
US-10-523-014-4  
; Sequence 4, Application US/10523014  
; Publication No. US20060094101A1  
; GENERAL INFORMATION:  
; APPLICANT: Lin, Lih-Ling  
; APPLICANT: Yannoni, Yvonne  
; TITLE OF INVENTION: MK2 Interacting Proteins  
; FILE REFERENCE: 08702-0097-00304  
; CURRENT APPLICATION NUMBER: US/10-523, 014  
; CURRENT FILING DATE: 2005-02-01  
; PRIOR APPLICATION NUMBER: USN 60/400, 044  
; PRIOR FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 915  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-523-014-4

Page 4

; TITLE OF INVENTION: Inflammatory Diseases  
FILE REFERENCE: P30\_1172-A USA CURRENT APPLICATION NUMBER: US/11/251,465  
CURRENT FILING DATE: 2005-10-14 PRIORITY APPLICATION NUMBER: 60/619,384  
PRIORITY FILING DATE: 2004-10-15 NUMBER OF SEQ ID NOS: 880  
; SOFTWARE: PatentIn version 3.3  
SEQ ID NO: 31 LENGTH: 919  
; TYPE: PRT ORGANISM: Homo sapiens US-11-251-465-31

Query Match 3.9%; Score 213.5; DB 7; Length 919;  
Best Local Similarity 21.7%; Pred. No. 3.9e-07; Mismatches 246; Indels 225; Gaps 34;  
Matches 160; Conservative 107; MisMatchers 246; Index 436

Qy 436 LKREPPELQOPISGAVIDPLSODPSVFNNSGVGSESESEHOTPDHLSPTASPVCRRTGSD 495  
Db 152 LTKKEE-----DNHTOCOLVPPVVEIGI-----SERONAEORTVOLMSTEPLPRTLSP 198  
Qy 496 TERQKQOSSGRTGGDDPGICSNSTDSTAQVLIGKKRLKAETL----- 540  
Db 199 TPSATSATPSQGIPSTD-----ESTPKK---SKARILESTIVSSLMATQPDPKGOGV 248  
Qy 541 -----ELSDLTVSKDKKDMSPPICTETBDQKQLT-----DICSNLBKEKLENR 586  
Db 249 GTGRSAKSLRQIAQVSPGPRD-SPAPFDSPWRRVLAIPLDNFTPTGSRTDSQVRH-- 305  
Qy 587 SLCCRSDPESPIKTSLSLSPTSKIGSYRSRDLAKKKASLR-----QTESDPDDR 638  
Db 306 -----SPITAPSPP-SVLAQKYS-----LVAKOSSVVRARRLAKKTYAEPAA-- 349  
Qy 639 TTLMADHSSKTVQH-----RLL-----SQREBELKERARVILLEQARRDAALKAGNK- 684  
Db 350 -----SGRICHSVYERLUNEVPKVGSKQKEPBEAEF-VAAAEPEVPGNGINS 400  
Qy 685 -HN-----TNTATPFCNRQ---LSDQDEDERRQLRERARQLTAERSGV 725  
Db 401 WPRNDTEIANSTPNPKPAASSPPTPSAQOEAKTDQADGPRESPPoSARRKRKYQA--- 456  
Qy 726 KNSELPSGEMAAEKLK-ERSKASGENDNIEIDTNEBIEPEGVGGDELTLNLDLT 784  
Db 457 -VSELDBEFOHLEBBLLOPPRSK-----PSSPCPASKVW-----RPLTFLHT 498  
Qy 178 PEONSKVLUKLKLUKVQPVQVANSPPSAQKAV-----TESSBQDM--- 826  
Db 499 VORNQNM-----TPSAPRSTMKSFKRNTPPLRMQPKEKERQRLENLR 542  
Qy 827 -KSGTEDLURTERLQKTTFRPNFVFWSKDSTVKTQLOFSOYIENPBMHQ---RS 880  
Db 543 RKEAEQOLRKVQEEDKRRRLEBVKRKEERLKV---LQARERVEQMKBKKKQIEQKFAQ 601  
Qy 881 IOEDTKIGNERKAITEQRKOSESEDDEVANKGKDTQSQVWGLAALLENBKQGIDTRALV 940  
Db 602 IDEKTEKAKEERLAEEKAKKK-----AAKMMEEYEARRKQB 638  
Qy 941 E-KRKLXILMDTGRTNTREBAMQBWFMVNKK-----NALIRMNQLSILKEHDLER-Y 994  
Db 639 EDARRLWQQ-----EEERRHQE--LLQKKEEBEERLRAAEEKLAQEERREQ 691  
Qy 995 BLANRELRAMIATEDWQTCRKEORREROLLDLSVALVANKRDLAVDIAQEKOAESEDEH 1054  
Db 692 ERREQRERQEERREQERREQERQERQERQERQERQERQERQERQERQERQERQ 751  
Qy 1055 LERTLQNGKRAKKEK 1072  
Db 752 LORELBEKK---KKEBQ 765

Query Match 3.7%; Score 202; DB 6; Length 2829;  
Best Local Similarity 18.1%; Pred. No. 1.2e-05; Mismatches 433; Indels 438; Gaps 52;  
Matches 225; Conservative 150; MisMatchers 433; Index 66

Qy 66 LDPPDEEDNEDDENRVMQBEKAKKITELINKNLFDE-----EKOLATVUNSNPFDPP 119  
Db 1134 VDYYDDDKTINNSERYSEBQDETERONQNKNKAYASEEHGEQDIDSYSKYSTDVS 1193  
Qy 120 AARLNPF-----GDDSEPRITETASPRKTEDSFNSTSNPKEVQTPQYLNPDEP 171  
Db 1194 SACKPSFPYNNNNSSQKPKCEQVSSNSNTPTSPNSNHRONQHPSAQSRPGLNRPQKIP 1253  
Qy 172 EARTIKUDSPPOSTKRNKR-----PVDMSKYLADSSKTBEELED-----ESN 215  
Db 1254 -----NKPSSINQDPIOTVQEDTPICFGRGSSLSSAEDDEGREENNSRGBSN 1305  
Qy 216 --PFYERK--SPPPNMLVNPNVOELETERRY-----K 245  
Db 1306 NTUQITEPERKEIISAVSKOGAVNNTSTRSSAHTRKRNQLQTSNISPDSRHKHQSVEFSSGK 1365  
Qy 246 AP-----APP----- 265  
Db 1366 SPSSRSGAQTPKSPPEHYVQETPLMFSPRCTSGSSLDSPFESHSTIASIASVABHMISGII 1425  
Qy 266 ASKLUSTSP-----KPSIIPSPVLRGRKNAQSOLLVWCKEVTKYRGKINTTS 316  
Db 1426 SSIDLPPSPGOMPPSPRSKTPPPQTQAKGGS-----VLSPKPGVMENTVS--- 1475  
Qy 317 WRNGLSFCALL-----HFRPDLIDYKSLNPQDIKENKKYDGF---ASTGIRULEP 367  
Db 1476 VNSAIQRVQVLORADTLHFA-----TESTPDGSCASSISALSIDEP 1518  
Qy 368 --SDMVLLIAIDKLTMTLYQIRAFSGOBILVVOIE---ENSSKSTVKGNTYEDT 420  
Db 1519 YQKDVLKIMPV-----ENDGDKNKAPEKEFIDNKAKKEDRSEGDIM 1565  
Qy 421 NSVDOQKFYAS---LSDLKREP-----BLOQPIGSA----- 449  
Db 1566 LPDTDDBDIILRECISAMPRIKPSRKVKPQPTGKPPVARKPSQLPVYKLSSQRN 1625  
Qy 450 -----VPFLSODD-----SVFVNDSGVGSESEHOTPDHLSPTASP 487  
Db 1626 LQTKHNFTHSDMPRWCYBGTGINSTATSLSDLTIESPSE-----PTNDQ 1676  
Qy 488 YCRTKSDTEPOKSQSSGRTGSGDPPGICSNSTDSTAQVLIGKKRLKAETLSDLVY 547  
Db 1677 NTDSLSTDPLBKRTDITPTEGR-----STDPTASKPNTPTVLDKAEEDGILA 1725  
Qy 548 S-----DKKKMSPPRICEETDBQKLQTLDIGSNIKEKLENRSLE-CRSDPSPK 599

Db 1726 BCIIHAMPKGKSHKPYRVKIMQ-----INTSAITSSGNSRSMOTDKRNPPTSPVK 1778  
 Qy 600 -----KTVLSPLSPKLGYSYSUDLAKKHHASLRQTESPDADETTIH 643  
 Db 1779 PNPQSCIPKPERLKNTTELKNPNSENOCIDPRK--PSSKKSQSKVANEKIPNNERETKGP 1835  
 Qy 644 ADHSKTIVOH-----LLSRQEEL-----KERRAVLLEQARDAALKA 681  
 Db 1836 AEDS--PHYHTPIEGTPYCFSRNDLSSLPFDDIDLSKEKABRKKGWTDOKV 1891  
 Qy 682 GNKHNTNTATPCNROLDQDDEERRSQL--BERRAROLIABARSGVKSSELPSYGYMAR 739  
 Db 1892 KYKHERAINPM-----GRQDQTPGKSLGGGRDOPKALV-----OKPTFSAAK 1935  
 Qy 740 KULKERSKASGBENDNIRIDNBRIPESPVVGGBLTLLENLDLTPEONSKULVULKLG 799  
 Db 1936 GTQDRGATDEKOMENFAI--ENTPVCP--SRNSLSSL-SDPQDNKKETPLK--- 1985  
 Qy 800 LEVQPOVANSASSAAQAVTSESDQMKSGTDLRTLRQKTERFRNPVUVVSDSTVRK 859  
 Db 1986 ---OTGTSETQGLRRPQTSGYAPKSFHVED-----TPVCFSRNSLSS 2026  
 Qy 860 TQLQFSQYIENRPEMRSQTSQEDTKKGNGNEKAIACTORTKPSDEDEVNLKPFKDTSQYV 919  
 Db 2027 LSIDSHEDDL-----OECISSAMPK-----KRKB-----KLNVEGKRSNSV 2065  
 Qy 920 VGBLALENEQKQDITRAALVEKRLVYMDTGRNTEERHAMQ---EWFMUWKKQAL 974  
 Db 2066 GGTLA--EPDPLDARDI-----QSDPSENAPSDSENPDWKALQEGANSI 2110  
 Qy 975 IRRMNQSLSLKEKEHDLERRYELNRLRAMLAEDWORTHEAQREQDILDEVAL--V 1031  
 Db 2111 VSRLHQMA-----AAGSLSRQGSSDSDSLISLKGSI 2141  
 Qy 1032 NKRDALVRLDAQEKQAEERDEHLERTLEQNKG--KMAKKEBKCVLQ 1076  
 Db 2142 SLGSPPFHILTBLKBK-----TITSNKGPKTLLPAEKSAL 2176  
 Result 7  
 ; Sequence 357, Application US/10505928  
 ; GENERAL INFORMATION:  
 ; Publication No. US20060088532A1  
 ; APPLICANT: Ludwig Institute for Cancer Research et al.  
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
 ; FILE REFERENCE: 28967/39178  
 ; CURRENT APPLICATION NUMBER: US/10/505,928  
 ; CURRENT FILING DATE: 2004-08-27  
 ; PRIOR APPLICATION NUMBER: US 6/0/363,019  
 ; PRIOR FILING DATE: 2002-03-07  
 ; NUMBER OF SEQ ID NOS: 866  
 ; SOFTWARE: Patentin 3.2  
 ; SEQ ID NO: 357  
 ; LENGTH: 3256  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-505-928-357  
 Query Match 3.4%; Score 185; DB 6; Length 3256;  
 Best Local Similarity 19.1%; Pred. No. 0.002;  
 Matches 231; Conservative 163; Mismatches 470; Indels 344; Gaps 52;  
 Qy 2 KOYASPMPT--OTDVK-LKFPLSKKWSMALOFLSCLCIFLRKGATDEDMOSLASIUS 57  
 Db 1172 KAMLTIPKPGADDEKIKAFMGTPVKQDLAGTIGS---KQLOQTPKEKAQALEDLAG 1226  
 Qy 58 MKQ-----AIGNLDPPBEDNDDD-----ENRVNQERKAAT-ELINKL 97  
 Db 1227 FKELFQTPGHTBELVAAGKTTKIPCDPSQSPDPVTPTSTKOPKRSRTRKADVEGELACR 1286  
 Qy 98 NFLDEAEKDLATVNNSMFDDPDAELNPNFGDDSEEPITE--TASPRKTEDSYNNNSYNN 155  
 Db 1287 NLMPSKGKAMHTPKPSVGKELDIIIP--VJTPVQKULDTENLIGSKRPQ-----TP 1336  
 Qy 156 PKEVQTPQYANPFD-----PEAVTK-----DSPQ-----STGRKNTRPV- 193  
 Db 1337 KEEQALEDLTGKEKFQTPGHTERAVAACKUTKPCESPPESADPTPTSTRQPKPE 1396  
 Qy 194 --DMARYLYA-----DSS-----KVEEELDESNPFPYEPKSTP 225  
 Db 1397 KRDVKELSLALKLUTQTSGITHTDKVPGGEDSKSINAFAREKQKULDPASVTGSKRPK 1456  
 Qy 226 PNNLUNPVQOL-----ETERYVKRKAAPPVPLSPKTC----- 257  
 Db 1457 TKEKAQPLEDLAGWKELFOPVCTDKPTTHKTTLKACRSQDPDVPIPTSSRPOSRSR 1516  
 Qy 258 -----VLENENTVSAGKLDSIPSPKPSIIPSPVPLGKRP-NASQSLIVWCKEVTRV 307  
 Db 1517 KVDVEEERPEFLKRTPSQAGMHT--PKPA-----VSGEKNUYAFMGTPTPVQKULDLTG 1570  
 Qy 308 VK-----ITMP-----TSWNRGLSPCATLHFRPDLIDYKSLN 342  
 Db 1571 SKRLLQTPKPKQALEDLAGPKELFQTRGHTBESMTNDKTVKACKSSQPDJ-----DKNP 1626  
 Qy 343 QDIKENKKAYDGFASIGISRLBLPSDMVLLAIPDQLTWMLYQIRAHSGQELNV-- 399  
 Db 1627 ASSKRKTVS--LGKVGV-----ELIAV-GKLT-----QISGETHTHTB 1665  
 Qy 400 VOIENNSKSTYKVSYNETTNSYDQEKYAELSDLKRSRBLQQPISGAUDFLQSODSV 459  
 Db 1666 PTGDOCKSMKAFMESPQKQILDSAASLTGSK--RQLTPKGSEVPDLAGFIE-----L 1716  
 Qy 460 FUNDGSVGVBESERHOT-----PDDHPLSPSTASPYCRT--KSDTOPO-----KSQO 503  
 Db 1717 FQTPSHTKESMNEKTKYVSYRASPDLVITPSSKQPQKSLRKADTEBFLAFRKQOTP 1776  
 Qy 504 SSGRSGSDPGICSNSTD-----QAOVTLGKRL-----KATTLE----- 541  
 Db 1777 SAGKAMHTPKPAVGBEKDINTPLGPVQKUDQPGNLPGPSHLRQLTRKEKAQALEBLTGF 1836  
 Qy 542 -----LSDIVVSDKKDMSPPFICBETDQKLQTLDIGSNLKEKLENNSLSLCRSDP 595  
 Db 1837 BLFQTPCTBPTADEK--TTKILKSPQS-----DPALPTNTKORPERSLIKADVE 1888  
 Qy 596 SPIKETSLSP-----TSLGYSYSD-----IDLAKKKHASPOTESPDA 637  
 Db 1889 BFLAFLRKLIPSAGKAMHTPKPAVGBEKDINTPLGPVQKUDQPGNLPGPSHLRQLTRKEKA 1948  
 Qy 638 RT-----TINAHDS--SKIVQHLLRSQER-----LKERRAVLLEQAR- 674  
 Db 1949 KALEDLAGFFRLFQTPGHTESMTDKITVSKSFQOPDPVKTSSKQRULKISLGKV 2008  
 Qy 675 RDAALKAGNHNNTATPCNROLDQDDEERRROLERAROLIABARSGVKSSELPSY 734  
 Db 2009 KEELVLPVGKLTQTSKQTHRETAG--DOKSKIKAFKESAKQMLDPPANGYGMERWPRTP 2066  
 Qy 735 EMAJEKLUKRS--KASGDENDNTIDNBRIPESPVVGCGDRLT-----ENDLDTPE 786  
 Db 2067 KEEAQSLEDLAGFKELFQTPDHTERSTD-----DKTTKLACKSPPPESMDPT 2115  
 Qy 787 QNSKLUDLKKLJLVEQPVANSASSAAQAVTSESDQMKSGTDLRTLRQKTERFR 846  
 Db 2116 STRRKPPTGKRD-----ELSAJQLOTOHTDVKPGDSDKGINVFRETAKOU 2168  
 Qy 847 NPVVKFSKDSVTVKTQLQSISSQYIENRPEMCR--ORSIQBTTKGNEKAAT----- 895  
 Db 2169 DPAASVTGSKRQTPKPKQPLEDLAGKELFQTPVCTDKPTTHKTTLKACRSQPD 2226  
 Qy 896 --TENRKESSEDEVNLKGFQKFTSQYVWGLAELNTEQOIDTRALVEKRLVYMDTGRN 953  
 Db 2229 VGTPTFKQPSKSLRK-----ADVERBESLAIARKRTPTPSVKGAMDTPKPGGD 2275  
 Qy 954 TEEBAMM 961

Db 2276 EKDMKAFM 2283

RESULT 8  
US-10-505-928-213  
; Sequence 213, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 213  
; LENGTH: 1120  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-505-928-213

Query Match 3.4%; Score 184; DB 6; Length 1120;  
Best Local Similarity 18.9%; Pred. No. 4.9e-05;  
Matches 232; Conservative 188; Mismatches 444; Indels 364; Gaps 56;

Qy 28 AALOFLSLCIFLREGKATDMDQSLASLUVSMQADIGN-----LDDPREDNEDDE 78  
Db 47 SLLPISLKLQG---SNSNPDVDFYNNKRDTSSERHFSKWLTCQHESRQPL 102

Qy 79 NRVNQBEKAKKIE-----LINKUNFLDAAEKO-LATVNS---N 113  
Db 103 DPTIQISSPKTSSEAVDPLIGNTWVLPSPLGQQDMTPEARLTWTMAETNSLING 162

Qy 114 PF--DDPDAELNP-FGD-----PDSEPRITERASPRITEDFYNNEYNPPEKVOY 164  
Db 163 PLRTDUDLVREEVARCMGDRPFSEVAVSEKPIFO-----ESPH 200

Qy 165 LNPFDPEPAAFTIKDSPOSTKRNKPVDMSKLYAASSKTREEU-DESNPPYRKS 222  
Db 201 L-----LRESPNPCSE---LHCSEKLSRSRTEAVFREDVPSSESNAPL-PSS 244

Qy 223 T---PPPN-----NLVNPVOBLETERRVKRKAPAPPVSPKPGVLMENTVSAGKD-L 270  
Db 245 VMLISPSLALADEFNRVHYDPEBEBIVENGAMEMEREMRPPTHPEKSETDQALVSSDIL 304

Qy 271 STSKPKSPST-----PSP-----VLRKPNASQSLIUVCKEVTKYRGKVKTNFTS 316  
Db 305 STCLTPNLVEMESOBAPGPAVEDVGRILSDTESWMSPLAWLB----KGNTISVMLEN 358

Qy 317 WRNGLSP-----CAILHIFRPLDIDYKSLNPDIKENKKAVDGASIG 360  
Db 359 LRDLSLSLPSMLRDLAIGTPFSTCSVGTVWFTPSA-----PROKSTWTSQT----GLVG 407

Qy 361 ISRLLEPSDMVLLAIPDKLTWMTLYQIRAHFSQELANVQIIFENSSKTYKVGNYETD 420  
Db 408 TKISTSETEQOLGGRPPDITALS-----RH-----DIAIDNT-----L 439

Qy 421 NSVYDQEKEYEALSDLKRPELQOPISGAQVDFLSQDDSVFVNDSGVGJESESTHOTPDL 480  
Db 440 SLVIVVEFLSRQJRDWKSQLANVHP-----ETQDSSQTDTSHSGITNKULQHLKESH- 491

Qy 492 -----EMQALAA-----RNWQSWVNLKSLK---SLL 518

Query Match 3.3%; Score 182; DB 6; Length 1384;  
Best Local Similarity 21.1%; Pred. No. 9.1e-05; Matches 206; Conservative 115; Mismatches 346; Indels 310; Gaps 42;

Db 575 LRGKDAARIVLEAPCAHSQRISQLEQDLSRMRPFGILKDMQTOVLGHAKQBVLVQQT 634  
Qy 631 ESPPADDTTLEHADHSSKIVQH---RLLSHOBELERARVYLEQA---RDAALKAGNK 684  
Db 635 VS-----LTTSQDWRSMOLDYTWTWALLSRSRQLTBLTVQSQAQERDVAE-EK 687

Qy 685 HNTNTATPCNQL-----SDQODEERROLERARQQLAEARSQGMSEPSYGENA 738  
Db 688 QEVSRVLQVSAQLECECIGTQEGLELENIRLATDLRQQLQIANMDSQKELQSOQHTCA 747

Qy 739 EKUKERSKASGDENDNITDNTBEPICFFVVGG-----GDBELNTBNDDPE 786  
Db 748 QDLAMKDRSILCQITQSNEQAAQCVKSEMAKHEQMABLQQQAVLAKEVARDIKEFAD 807

Qy 787 QNSKL-----VDLKLUKLEVQPOVANSPESAQAKVTESSEDQMKSGTEDLRTRLQ 839  
Db 808 QENOVAHILGLGOVECQLKITLEVLRB--RSLOCENLKVTVENLTAKLUSTIADNQEQDQE 865

Qy 840 KITERPRPVVPSKOSTRTKQLOSPQSYIENRPEMKQRSIQBDTIGKNEKAATETQ 899  
Db 856 KTRO-----VSOKLGLITEOLQSLTFLOTK-----LGEKTSGETBLUSTA 906

Qy 900 RKPSDEBVNLKGPKDTSQVVBELAALNEQ-----KQIDTR-AALVEKLRV 946  
Db 907 CPPTOEHFL---PNDRTPLGSITAVADEEERBTFPVPLLGDSKAFTRVAKVSLO-- 959

Qy 947 LMDTGRVTEEEBAMMOMFVPLVKNNAIIRRNMOLSLVKEKDLERREYELLAR--EIRLA 1003  
Db 960 ---PAETPGMBSLAEKNSIMTTELQSL-----CSLQESK---EARLTIQRKICBLQA 1007

Qy 1004 MLAXEDQKTEQKRE-----QLL-----DELVALVNRKDALVRDQDAQK-QA 1048  
Db 1008 RLQNEBHQEVQAKADEKIKUNQALCILRYKNEKBLQEVQNEKILEQIDKSGELSL 1067

Qy 1049 EERUBHLERTBONKGKAKGEGKCVLQ 1076  
Db 1068 REFWTHLRLS-----RRAETETK-VLQ 1089

RESULT 9  
US-10-505-928-799  
; Sequence 799, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 799  
; LENGTH: 1384  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-505-928-799

Query Match 3.3%; Score 182; DB 6; Length 1384;  
Best Local Similarity 21.1%; Pred. No. 9.1e-05; Matches 206; Conservative 115; Mismatches 346; Indels 310; Gaps 42;

Qy 162 PQLNPDPDEPAAFTIKDSPOSTKRNKPVDMSKLYAASSKTREEU-SNSTPKSPIP 221  
Db 161 PPSPSPVRAESELSVNGHNTPOTRGRS--ACASHSLSVSIKEQLEIMDSLVRBPG 217

Qy 222 STPPPNVLNVNPVOBLETERRVKRKAPAPPVSPKPGVLMENTVSAGKD-STSPKSPIP 280  
Db 218 AAQKKPAPATSLPSLPMANGRY-----LISRPT---SPGAMSVQSSYENTSPAPSPLS 266

Qy 281 SPV-----LGKPKNASQSLIUVCKEVTKYRGKVKTFNPTSWRNGLSPCATLHFP 330









APPLICANT: Rosenberg, Steven  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
 FILE REFERENCE: 50661200104  
 CURRENT APPLICATION NUMBER: US/10/511,937  
 PRIOR APPLICATION NUMBER: PCT/US2003/012946  
 PRIOR FILING DATE: 2003-04-24  
 PRIOR APPLICATION NUMBER: US 10/131,831  
 PRIOR FILING DATE: 2002-04-24  
 PRIOR APPLICATION NUMBER: US 10/325,899  
 PRIOR FILING DATE: 2002-12-20  
 NUMBER OF SEQ ID NOS: 3117  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 2566  
 LENGTH: 1186  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-511-937-2566

Query Match 3.0%; Score 162.5; DB 6; Length 1186;

Best Local Similarity 18.4%; Pred. No. 0.0015; Mismatches 417; Indels 395; Gaps 53; Matches 221; Conservative 167; Mismatches 417; Indels 395; Gaps 53;

Qy 2 KQYASPMPTODVKUKPKPUSSKKVVAHSALOFLSLCIFLRREGKATDEDMOSLAVLSMKOA 61  
 Db 95 KDLASSDRCTTEKULKTPLKQATKAFR-----SKDEALSLITQ---RREN 141  
 Qy 62 DIGNLDDFERD---NEDDDE---NRVNQDEBKAAKITELINKUNFLDEAKLAVTNSN 113  
 Db 142 DLYVLPPLQBEKHSSEEDKEWOMNO---KOALQSFPHNPOAIDIESBDSSL---196  
 114 PFDPPDAEILANPFGDPDSERPIBT-----TASPRKTED-----146  
 Db 197 --PPEV-----KHBLTDMKEFTKRRTLFTEAMPEBESDFSQYOLQGLLKKNTL 243  
 Qy 147 -----SFYNNSYNPFKEVQTPOYLNPFDEPAFTVKIDSPPPOSTK 186  
 Db 244 NOHLEHVQKEMNQHQHSIGHTRRQYEDEGEFLKEVSRRVS---EDPSHYTLKGIOAKTV 301  
 Qy 187 RKNTRPVDMSKYLYADSSKTYREBEELESNPYPYKSTPP--PNLY-----NPVQEL 236  
 Db 302 EVDSELSPSSSKMFGMSFDVUSSPCKLKTKKEPDATPPSRTLLAMOALLGSSSEEL 361  
 Qy 237 ETEREVK---RKAPA-----PVLSPKPGVLEN---TYSACKDLSTS PKSPIPSP 282  
 Db 362 ESENKRQARCRNAPAVDEGSISPRTLSA KRALDDDEDVKAQDVG---412  
 Qy 283 VLGKPNASOSLVLWCKEVTKNY-RGVKLTNFTSWRNGLSPCATLHFRPDLDYKSJN 341  
 Db 413 ---GPGAEEMR---NSSPNSDEGLKVRD---GKJGPPTATLAS-----SSON 452  
 Qy 342 PQDIKENNKCKAYDGFASTGIGSLRLPSDMWTLATAIDPKLTWTYLYOIRAHFFSGOBINWQ 401  
 Db 453 -----SBERVASTNEGR--BPTDSV-----PKCOMSLVR 480  
 Qy 402 IEEENSSKSTVKGNYETDTNISDVQDKPYAELSLDKRPELQLQPIGAVDPLSODDSVRF 461  
 Db 481 -----VGTAEF--PISD-----ESMKDRKDRPLSAVR 509  
 Qy 462 NDSGVGESESEHQIPDDHLSFESTASPYCRTCSDTEPKQSQQSSRTGSDDPGICNTD 521  
 Db 510 HSDARGLPLNBRBLTP-----ASPTCMTNSVSK-----537  
 Qy 522 STOAOVLGKCRKLKARTLSDLVSDKCKDMSPPPICRTEDSOKLQTIDIGSNLEK 581  
 Db 538 -THARVLEQOMBLCYEYESKFDSLSSSDATCKCDNSASEFIVGPVSLOSTTSIVSVPSA 596  
 Qy 582 LENSRSLECRSSDPSPIKKTSLSPIGKGSYSRDLARKKHASLQTBSPPADRTL 641  
 Db 597 VDNVENV-----VSFNKEHENFLETOEQQTESAG 628  
 642 NHADHSSKIYQHRLLSROEBLKERARVILLEQARRDAALKAGNKINTNTATPPFCNRQLSDQ 701

Search completed: May 20, 2006, 17:30:35  
 Job time : 18 secs

Db 629 QDLISIPIKAVEPMEIDESSESDESASPTEQVSVIDEELQA-----EPPESTKPPSEQ 680  
 Qy 702 QDEERRRQLRERAROLIAERARSQYKMSCEPSYGENMAKURSKASGDENDNIEIDNE 761  
 Db 681 GEER-----LV-----GTRERAPAESISSLRONSERDODVG-EPOBAEKAED 723  
 Db 762 BIEGFVUGGGDELNLNDTPBONSKLUDLKK-----LLSEVO----803  
 Qy 724 SLHEWQDI-NBLELTESLNL-LAQONS---LKAQKOOBRIAATVGMPLRSQELL 777  
 Qy 804 ----POVANSPSSIAQAKATESSRQDMKGSTEDEIRTERLOKTTFRNPVVFESKIDVTK 859  
 Qy 882 PGHGLPLKFESEWWHAEQKNPKTRPNPDTKVKKRLQLTPOFPNPAVAEYLKP-- 939  
 Db 911 ---GFKDTSOVYGBLALENNEQKOIDTRALVERKLRYMDTG--RNTEBEEAMMQENF 965  
 Db 940 -VVDSSKG-----SFLWKGPDLKDUTKIRFCQYF-----GMNRT---KTDLSF-- 978  
 Qy 1026 ELVALVNKRDLVRLDQEKQ-----ABEDDEHLERTLBONKGK--MAKKESK 1072  
 Db 979 -----PVKQLDAAQTOLRIDSPFRLAQKEBEDKRIKSORLAVTCMLRKKE 1028

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Qy 1051 BDEKLERTEEQNKGRMKAKEEK 1072  
Db 1014 LQSOLNEOROQNSQNLSEKDQQ 1035

RESULT 3

S28381 urophin - human  
N: Alternative names: dystrophin-related protein  
C: Species: Homo sapiens (man)  
C: Date: 17-Apr-1993 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004  
C: Accession: S28381; S28914; S03966  
R: Tinsley, J.M.  
submitted to the EMBL Data Library, November 1992  
A: Reference number: S28381  
A: Accession: S28381  
A: Molecule type: mRNA  
A: Residues: 1-3433 <TIN>  
A: Cross-references: UNIPROT:P46339; UNIPARC:UPI000013786A; EMBL:X65086; NID:934811; PIDN:R7TINSLEY; Blake, D.J.; Roche, A.; Fairbrother, U.; Riss, J.; Byth, B.C.; Knight, Nature 360, 591-593, 1992  
A: Title: Primary structure of dystrophin-related protein.  
A: Reference number: S28914; MUID:9306045; PMID:1461283  
A: Accession: S28914  
A: Molecule type: mRNA  
A: Residues: 2994-3435 <LOV>  
A: Cross-references: UNIPARC:UPI000000673; EMBL:X15498; NID:930933; PIDN:CAA33515\_1; PID:503966  
A: Molecule type: mRNA  
A: Accession: S28914  
C: Comment: This protein is found primarily at the neuromuscular junctions in adult muscle regenerating muscle.  
C: Genetics:  
A: Gen: GDB:UTRN; DMDL  
A: Cross-references: GDB:119851; OMIM:128240  
A: Map position: 6q24-6q24  
C: Key-words: actin binding; cytoskeleton; leucine zipper; membrane-associated protein; microtubule-associated protein; spectrin/dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrophin repeat homology <ACT>  
C: Superfamily: dystrophin; alpha-actinin actin-binding domain homology <ACT>  
F: 3108-417/Domain: spectrin/dystrophin repeat homology <SP01>  
F: 418-526/Domain: spectrin/dystrophin repeat homology <SP02>  
F: 528-637/Domain: spectrin/dystrophin repeat homology <SP03>  
F: 638-885/Region: hinge  
F: 686-796/Domain: spectrin/dystrophin repeat homology <SP04>  
F: 804-902/Domain: spectrin/dystrophin repeat homology <SP05>  
F: 906-1013/Domain: spectrin/dystrophin repeat homology <SP06>  
F: 1015-1121/Domain: spectrin/dystrophin repeat homology <SP07>  
F: 1124-1230/Domain: spectrin/dystrophin repeat homology <SP08>  
F: 1233-1334/Domain: spectrin/dystrophin repeat homology <SP09>  
F: 1339-1450/Domain: spectrin/dystrophin repeat homology <SP10>  
F: 1451-1541/Domain: spectrin/dystrophin repeat homology #status atypical <SP11>  
F: 1543-1649/Domain: spectrin/dystrophin repeat homology <SP12>  
F: 1651-1755/Domain: spectrin/dystrophin repeat homology <SP13>  
F: 1856-1973/Domain: spectrin/dystrophin repeat homology <SP14>  
F: 1975-2081/Domain: spectrin/dystrophin repeat homology <SP15>  
F: 2083-2185/Domain: spectrin/dystrophin repeat homology #status atypical <SP16>  
F: 2227-2333/Domain: spectrin/dystrophin repeat homology <SP17>  
F: 2335-2440/Domain: spectrin/dystrophin repeat homology <SP18>  
F: 2442-2556/Domain: spectrin/dystrophin repeat homology <SP19>  
F: 2558-2688/Domain: spectrin/dystrophin repeat homology <SP20>  
F: 2798-2869/Region: hinge  
F: 2812-2849/Domain: WW repeat homology <WW1>  
F: 2837-3117/Region: cysteine-rich  
F: 3263-3284/Region: leucine zipper motif  
F: 3328-3349/Region: leucine zipper motif

Query Match 5.9%; Score 326.5; DB 1; Length 3433;

Best local Similarity 19.8%; Pred. No. 6.4e-06; Indels 303; Gaps 37; Matches 197; Conservative 159; Mismatches 336;

Qy 285 RKPNAQSULWCKEVTKNYRGKINTITSWANGSLTCALLHFRPFLDYLKSINPRPDI 345  
Db 148 QTMSEKILISWTRQTWPSQTVNLNTMSWTDGLATNAVLRHKPLFSWOKVKKNSP 207

Qy 346 KENNKKAVGPGAS-IGSRLLESDMWVIAIPDKLTWMLYQI----- 388  
Db 208 IERLHAKSAQTYLGKILBD-VAVRLPKSKSIIMYLISLFEVPPQVTTDAIREV 266

Qy 389 ---RAHFSQELANVQTEENSSKSTYKVGYETD--TNSSYDQEKKYAEELSDLKRPE 441

Db 267 ETLPKYKKGCEBAINIQSTARBEHRSRPAETPSTTEVDMDLSYQIALEV---- 321

Qy 442 LQPPISGAVDLSQDDSTFVNDGGESSESHOPTDPLSPASP-----Y 488

Db 322 LTWILSADPTFQEDD--ISDD--VEETQFMATHEATMELAHQSSVGSVQAGNOI 377

Qy 529 LGKERRLLKARTBLSD-----LYVSDKKKOMSP 556

Db 436 LTBERIQWMETCPIDDVYKSLQKLESHKSLQSDLEARQVKVNLTHAVVIDENSGSA 495

Qy 557 PFT-----CEBTQ-BLQTLDIGSNREKEKLNRSLECRSDPESIK 539

Db 378 TQGTLSPDRPEPELQRQMTLARWEALRVESMQRSRHD-VLMELQKQLQQLSAMIT 435

Qy 496 TAILEDQLOQGLGERWTAVCRWTERWNLHQLI-----IWOELFE---OCLIKAWLTK 548

Db 600 KTSISLPTSKGYSYSRDIDLAKKHASTQTESDPADRTTINHADHSKIV----- 652

Qy 549 BEALNKVQTSNFQDKERSVSVRRAILKE--DMEMRQTL--DQSBIGDVQQLD 602

Qy 653 -----HRUJSRQEHLKER-----AVTLLSQR-RUA 678

Db 603 NSKASKKINSDSBSLTQWLDSSNQVTOAVKUGMSQIPQDQLETPVVRQA 662

Qy 679 LKAGNKHINTATPPCNQQLSDQDERRQRLERARQL--IAEARSGKMSSELSPGCR 735

Db 653 ITKSKQSLUPPPPKQKQI-HVDIBAKKFAIASALNNLWKWKAQIT'VEKEM 720

Qy 736 MA-AEKLAERKSKASGDEENDNIEILDNEPIPEGFVVGCGDBLNLENDIDTPQENSKVL 794

Db 721 MDTSEMKGKLKA-----LEGEOREIPR-----ABELNGTGQJYBQMKGEGIPE 767

Qy 795 KLUKLUETOPQVANSPPSSAAQKVTTESSBDMKGSTEIDRTERLQKTERFRNPVUFKRD 854

Db 768 EIKNVLB-----KVSEBWKNVSQHLDLERK-----IQLOED 799

Qy 855 STVKTKQJOSFSQYIENPREMKRQSQDFT-----KGHEEK 892

Db 800 INAFKQJQDLEKVKITGEWVKTSISSESSRSLPSLSDSCORELTNLGJPKIENR 859

Qy 893 AATETTORKPSDEDEVNKG-----KDTISQYVVGELAALNEQKQIDTRA 938

Db 860 ASCSALM-QPSA-PDFVQGFDFSLFLGRYQVAQEAVEDRQH-----LENELKGQGPGRAY 912

Qy 939 LVERKLRYLMDTGRNTR-----EREMAMQEWFLVNUNKONALTRM 978

Db 913 L-EETLKTKLKVANDSEKNAQVSILVNLAKYETKALQKKTIDE--I LENOKPALKLIA 968

Qy 979 NOISLKE--EHOLERRELLERLRAALAEWQKTAQKRRQQLLDELV----- 1028

Db 969 EETKALKKVNHPYVEKLTQFUDVOG---KNNKQVLYKSLDHLEFIALTAREA 1023

Qy 1029 --ALVNRKDADLDAQKQABEEDSHLERTLEQ 1061

Db 1024 DSTVIKMDGVKDFLMMQQAQGDDAGLQLDQ 1058

T34418 hypothetical protein F12F3.3 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C;Accession: T34418  
 R;Puton, B.; Wohldmann, P.  
 submitted to the EMBL Data Library, July 1998  
 A;Description: The sequence of *C. elegans* cosmid F12F3.  
 A;Reference number: Z21521  
 A;Accession: T34418  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-3488 <FULL>  
 A;Cross-references: UNIPARC:UPI000017B8E6; EMBL:U80022; PIDN:AAC25885.1; GSPDB:GN00023;  
 A;Experimental source: strain Bristol N2; clone F12F3  
 C;Genetics:  
 A;Gene: CESP:F12F3.3  
 A;Map position: 5  
 A;Introns: 281/3; 332/1; 562/3; 600/3; 1866/3; 1944/3; 3393/1  
 Query Match 5.9%; Score 324.5; DB 2; Length 3488;  
 Best Local Similarity 19.1%; Pred. No. 8a-06; Mismatches 429; Indels 397; Gap 54;  
 Matches 245; Conservative 215; Mismatched 429; Indels 397; Gaps 54;  
 Qy 25 VNSALQFPLSLCIPFLRSKATPDQMQLASLISMQADIGNDD--PEEDND-DEENR 80  
 315 VAGEBAWCPFDVVMHSE-ESRD--D----KSVDEVTDSTVLEBKDKGDKSK 361  
 Qy 81 VNGEEKAQAKTILELINKUNFLDAEQLATVNNSPFDDDAEELNPFGDPDSEPIETAS 140  
 362 PRTKKKIKKKG-TPEBQVTAEPPEQOKISVUDQVAETIVGAKKKPDAKPK-TDLISK 419  
 Qy 141 PRKTEDSFYNNSYNPFPKEVQTPQYLNPDEPRAFTVTD--S-PROSTKRKNR 191  
 420 AKKDSKS-----KVSDEPHASTEERKSTTRKPTNDKTISKSAEKKV 461  
 Qy 192 PVTMSKLYADSKTEFELDSNPFPKSPTPPPNNVLVNPVOBLETERRVYGRKAP--- 247  
 462 PKKEVTKPLEAKKPKVDDKDAQSOPSSKESPP-----TDGKKKQIQIPALF 509  
 Db 510 IPDEISSLRFG-----DPSMTMSETNTITIRGREGSSADAKPVL-----EPISAVY 555  
 Qy 307 GVKITNFTTSWANGLSFCATILHIFRPD-----LIDYKSHNPQD-----IKE 347  
 Db 556 SMVKVFTLVESAKEKAERFSKRSRSETPDOKSRKKEGLPAKESKEKKDDEBTABQSTEALIE 615  
 Qy 348 NNKKAVDGFAIGISRLR--PSD--MULLAIDKLTWMTLYQIRAHFSGQEL--NNV 400  
 616 SKRKEVDE-----SKIEQQPSDKNSKKEWVGWPEKA-----AGPETKKDV 656  
 Qy 401 QIENEENSKSTYKVGNVETDTNSVQDFKPYFALSIDLKREPELQQPISGAVIDFLQDSVF 460  
 657 EIEEVPKKTTKTKTKESD--SISQKSNLVPAD-----DDKSKEDDV- 698  
 Db 461 VNDSGVGESESEHQTPDHLSSTASPYCRRTSRDKSDTEPKQKQOSSGRTGSDDPGICNT 520  
 699 -----TDKSKKTRBDQTKWDS-----KLEKAADTQKIEETVVDK----- 737  
 Qy 521 DSTOAGVTLGKRLKAKTLESLDLYVSKDKKDMSPPI---CESTDQOKQLT----- 571  
 738 -----SKKVKVKKT-EKSDPSLQSKB--TPPVVEPTPKPARSEAOKIAEVNACK 785  
 Qy 572 --DIGSNELEKEGLNSRL--ECSRDPESITKTSIUSPTSKLGKYSYSDLDLAKKKHAS 626  
 786 QKEVDNLKREAEVAAKTIADEBLKIEEAANIKKA-----EYAAKKQKEK 832  
 Db 627 LROTESDPD-----ADRTTINHADHSKTVWHLRSRQEELKERVILLEQARDDA- 678  
 833 DEQLKLETEVVSKSAEAKLELQAOQIKKALADAVKKQELNEKNK--LEAAKSAAD 890  
 Qy 679 -----LKAGNKHNTNTATPFQNRQL-----SDQQDE 704

RESULT 5  
 PADA  
 alpha-actinin - slime mold (*Dictyostelium discoideum*)  
 C;Species: *Dictyostelium discoideum*  
 C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 09-Jul-2004  
 C;Accession: S00103; A29006  
 R;Noegel, A.; Witke, W.; Schleicher, M.  
 FEBS Lett. 221, 391-396, 1987  
 A;Title: Calcium-activated non-muscle alpha-actinin contains EF-hand structures and high  
 A;Reference number: S00103; MUID:87304850; PMID:3622778  
 A;Accession: S00103  
 A;Molecule type: mRNA  
 A;Residues: 1-862 <NOE>  
 A;Cross-references: UNIPROT:PO5095; UNIPARC:UPI000015099; EMBL:Y00689; NID:9717; PIDN:  
 R;Witte, W.; Schleicher, M.; Lottepeich, F.; Noegel, A.  
 J. Cell Biol. 103, 969-975, 1986  
 A;Title: Studies on the transcription, translation, and structure of alpha-actinin in Dic  
 A;Reference number: A29006; MUID:86304574; PMID:3745276  
 A;Accession: A29006  
 A;Molecule type: DNA  
 A;Residues: 92-359, 'P', 361-500, 'T', 502-505 <WIT>  
 A;Cross-references: UNIPARC:UPI000016B8E8; EMBL:X04324; NID:97202; PIDN:CMA27855.1; PID:  
 C;Superfamily: alpha-actinin; alpha-actinin actin-binding domain homology; calmodulin rel  
 C;Keywords: actin binding; calcium binding; duplication; EF hand; homodimer  
 F;21-236/Domain: alpha-actinin actin-binding domain homology <ACT>  
 F;266-377/Domain: spectrin/dystrophin repeat homology <SP1>  
 F;386-493/Domain: spectrin/dystrophin repeat homology <SP2>  
 F;505-607/Domain: spectrin/dystrophin repeat homology <SP3>  
 F;616-717/Domain: spectrin/dystrophin repeat homology <SP4>  
 F;736-762/Domain: calmodulin repeat homology <EF1>  
 F;766-798/Domain: calmodulin repeat homology <EF2>

Query Match 5.8%; Score 321; DB 1; Length 862;







401 ENERQVAILAELOQREKQKUQLQAFHKK----AKLRSWLSRVQVVLSEMEMERSASQV 455  
Db :  
Qy :  
531 KRULLKASTLESDLYVSDKKOMSPPPICEDEBOKLQTDLGNSLNLEKKEKLNSRSLEC 590  
Db :  
C;Accession: T23630 ; T24242  
R;Kershaw, J  
A;Cross-references: UNIPROT:O02425; UNIPARC:UPI00017CF3B; EMBL:281570; PIDN:CA04608.1;  
A;Reference number: 219774  
A;Accession: T23630  
A;Status: preliminary; translated from GB/EMBL/DDJB  
R;Lennard, N  
A;Submitted to the EMBL Data Library, July 1996  
A;Reference number: 219862  
A;Accession: T24242  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: DNA  
Query Match 5.8%; Score 316.5; DB 2; Length 4101;  
Best Local Similarity 20.3%; Pred. No. 2.1e-05;  
Matches 204; Conservative 150; Mismatches 353; Indels 297; Gaps 41;  
A;Map position: 5  
A;Introns: 29/3; 89/3; 184/3; 312/3; 812/2; 1461/3; 1531/3; 2050/2; 2413/2; 2466  
Db :  
Qy :  
591 RSDRESPIKTSLSPSKQYSRDLIACKKASLRQTESDADRTLNHDHSKI 650  
Db :  
Qy :  
514 LLBQ----RKRALMSLNDL-MSLJRDITLSNEVSYLSPAVNRDVGHKLIGVDELGK- 557  
Db :  
561 VORHLLRSQ----EELKERARVILLE----QARRDAALKAGNKHNNTATPP 693  
Db :  
566 -HDILDAQINAHGSLLSKUSQANYIRHKESQDFDVLQRKDVT-----QINTLVEL 620  
Db :  
694 CNRQLSDQDQEERRRQLRERAROLIAEARSGVMSLEPSYGENA---AEKUKERSKASG 749  
Db :  
621 C-----RSRRLGLERARSLSFQVQDHES----EMAWLAKEKEKLCCTALNSG 662  
Db :  
750 D-----ENDNIEIDTNBIEPEGFVWGG----GDELTLNLENDL-----782  
Db :  
663 DISAVPQTLLIVKVNEMEMOTHWARSKGMIGGGERLVONGQSKEDIORRITOMHRWERL 722  
Db :  
783 -----DTPEONS-----KLVL-----794  
Db :  
723 RVAVDALGNWLSEARHAAQYFODANAEASWIREKPLVKSDDLGGRDEGAESLIIQRHARL 782  
Db :  
795 -----KLUKLULEVQPVANSFSSAAQAKVTESSQDMKSCTEDLERTERLOKTTBRP 845  
Db :  
783 EEEIRAYKSDISRLRLEMOSQLAN--SAFTHTATTSQSVOE---TEEVNPQVEMSYNVE 835  
Db :  
Qy 845 RNPVVFPSKOSTVTKTQLOPSFSQYIENPE---MKROR-----SIQB 883  
Db :  
836 GNGMRVSKGEVLLALE-----KSTPEWWRALKDGTDGEGYVANYCKIVPGETVTVQ 887  
Db :  
884 DTKK-----GNEEKAA-ITETORKPSDEDEVLKGFQTSQVNG-----ELAAL 926  
Db :  
888 TTOKTTLLEGNETKSSVVAQDRQHKTISNDYRELKLADVRRLISDNITKLRFYRECDEF 947  
Db :  
927 ENEQKQITDRAALVEKRLYLMGTGRNTBEAMMQEWMLVNNKNAIRRNMQLS--LL 984  
Db :  
948 ERMAKEIYVSLA-DEPSBEHVAFLRKFDKLEADMK----TNGGTQQLKHINDIANDLI 1000  
Db :  
Qy 985 EKEHDLERREYLNAREJALMAATEBDWKTEAQKRERQQLDILVALVNRDALVRDLDQA 1044  
Db :  
1001 SEGHGQSKRKEVROHKINAM----WDNWLRLRKGQYRLE---ATER--VADFFTT 1047  
Db :  
1045 EKEGBE-----EDHEUERTLQNGKOMAKKE 1071  
Db :  
1048 CESAREWWLISKFEPQDNRNDVKSQNLONLERDLKPLEDKIAALEK 1091  
Db :  
RESULT 10  
T23630 hypothetical protein R31.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
Db :  
R;Kershaw, J  
A;Cross-references: UNIPROT:O02425; UNIPARC:UPI00017CF3B; EMBL:281570; PIDN:CA04608.1;  
A;Reference number: 219774  
A;Accession: T23630  
A;Status: preliminary; translated from GB/EMBL/DDJB  
R;Lennard, N  
A;Submitted to the EMBL Data Library, November 1996  
A;Accession: T23630  
A;Molecule type: DNA  
A;Reference number: 219862  
A;Accession: T24242  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: DNA  
Query Match 5.8%; Score 316.5; DB 2; Length 4101;  
Best Local Similarity 20.3%; Pred. No. 2.1e-05;  
Matches 204; Conservative 150; Mismatches 353; Indels 297; Gaps 41;  
A;Map position: 5  
A;Introns: 29/3; 89/3; 184/3; 312/3; 812/2; 1461/3; 1531/3; 2050/2; 2413/2; 2466  
Db :  
Qy :  
591 RSDRESPIKTSLSPSKQYSRDLIACKKASLRQTESDADRTLNHDHSKI 650  
Db :  
Qy :  
514 LLBQ----RKRALMSLNDL-MSLJRDITLSNEVSYLSPAVNRDVGHKLIGVDELGK- 557  
Db :  
694 CNRQLSDQDQEERRRQLRERAROLIAEARSGVMSLEPSYGENA---AEKUKERSKASG 749  
Db :  
621 C-----RSRRLGLERARSLSFQVQDHES----EMAWLAKEKEKLCCTALNSG 662  
Db :  
750 D-----ENDNIEIDTNBIEPEGFVWGG----GDELTLNLENDL-----782  
Db :  
685 DISAVPQTLLIVKVNEMEMOTHWARSKGMIGGGERLVONGQSKEDIORRITOMHRWERL 722  
Db :  
783 -----DTPEONS-----KLVL-----794  
Db :  
745 RVAVDALGNWLSEARHAAQYFODANAEASWIREKPLVKSDDLGGRDEGAESLIIQRHARL 804  
Db :  
Qy :  
795 -----KLUKLULEVQPVANSFSSAAQAKVTESSQDMKSCTEDLERTERLOKTTBRP 845  
Db :  
805 EEEIRAYKSDISRLRLEMOSQLAN--SAFTHTATTSQSVOE---TEEVNPQVEMSYNVE 857  
Db :  
846 RNPVVFPSKOSTVTKTQLOPSFSQYIENPE---MKROR-----SIQB 883  
Db :  
858 GNGMRVSKGEVLLALE-----KSTPEWWRALKDGTDGEGYVANYCKIVPGETVTVQ 909  
Db :  
970 ERMAKEIYVSLA-DEPSBEHVAFLRKFDKLEADMK----TNGGTQQLKHINDIANDLI 1022  
Db :  
Qy :  
985 EKEHDLERREYLNAREJALMAATEBDWKTEAQKRERQQLDILVALVNRDALVRDLDQA 1044

Db	1023 SFGHGGSRKTVROHKINAM-----WDNLERLKKORGVRIL-----ATER---VADFDTT	1069	R; Speicher, D.W.; Marchesi, V.T.
Qy	1045 EKQABE-----EDSHHLRTEQWKGKMAKKEE	1071	Nature 311, 177-180, 1984
Db	1070 CESARWMLSLSKPQLDRNPNDVKSLQNLRLPKPDKIALEK	1113	A; Title: Erythrocyte spectrin is comprised of many homologous triple helical segments.
RESULT 11	SJHUB		A; Reference number: A93341; MUID:84295638; PMID:6472478
C; Species: Homo sapiens (man)	C; Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004		A; Accession: B27016
C; Cross-references: UNIPARC:UPI000173DBB; UNIPARC:UPI000173DBC; UNIPARC:UPI000173DBD;	C; Cross-references: UNIPARC:UPI000173DBB; UNIPARC:UPI000173DBC; UNIPARC:UPI000173DBD;		A; Molecule type: protein
C; Note: the purified protein had a blocked amino end	C; Comment: Spectrin is a major structural component of the erythrocyte membrane cytoskeleton		A; Residues: 292-324, 'X', 326-329, 'Y', 331-332, 434-532, 718-734, 'V', 736-773, 'X', 773-777, 1036
C; Reference number: A37064; MUID:90307707; PMID:2195056	C; Genetics:		A; Cross-references: 1994-1997 <SPB>
A; Molecule type: mRNA	A; Gene: GDB:SPB		A; Map Position: 14023-->4923
A; Residues: 1-2137 <WIN>	A; Cross-references: GDB:119602; OMIM:182870		C; Superfamily: spectrin beta chain; alpha-actinin actin-binding domain homology; spectrin; heterodimer; membrane
A; Cross-references: UNIPARC:UPI000135DB5; GB:J05500	A; Map Position: 14023-->4923		C; Keywords: actin binding; cytoskeleton; actin-binding domain homology <ACT>
A; Note: the authors translated the codon GAG for residue S56 as Arg, CAC for residue 801	R; 636-741/Domain: spectrin/dystrophin repeat homology <SP02>		F; 55-271/Domain: alpha-actinin actin-binding domain homology <SP01>
R; Winkelmann, J.C.; Chang, J.G.; Scarpa, A.L.; Marchesi, V.T.; Forget, B.G.	R; 742-846/Domain: spectrin/dystrophin repeat homology <SP04>		F; 301-412/Domain: spectrin/dystrophin repeat homology <SP01>
J. Biol. Chem. 265, 1187-1182, 1990	R; 1167-1272/Domain: spectrin/dystrophin repeat homology <SP03>		F; 421-526/Domain: spectrin/dystrophin repeat homology <SP02>
A; Title: A splice site mutation of the beta-spectrin gene causing exon skipping in hered	R; 1273-1377/Domain: spectrin/dystrophin repeat homology <SP05>		R; 637-735/Domain: spectrin/dystrophin repeat homology <SP04>
A; Reference number: A39346; MUID:91332035; PMID:1840591	R; 1378-1476/Domain: spectrin/dystrophin repeat homology <SP12>		F; 1160-1166/Domain: spectrin/dystrophin repeat homology <SP01>
A; Accession: A39345	R; 1583-1688/Domain: spectrin/dystrophin repeat homology <SP13>		F; 1167-1272/Domain: spectrin/dystrophin repeat homology <SP03>
A; Molecule type: DNA	R; 1689-1791/Domain: spectrin/dystrophin repeat homology <SP14>		F; 1273-1377/Domain: spectrin/dystrophin repeat homology <SP12>
A; Residues: 2002-2137 <GNA>	R; 1792-2007/Domain: spectrin/dystrophin repeat homology <SP15>		F; 1378-1476/Domain: spectrin/dystrophin repeat homology <SP12>
A; Cross-references: UNIPARC:UPI000173DB5; GB:J05500	R; 2008-2118/Domain: spectrin/dystrophin repeat homology <SP17>		F; 1583-1688/Domain: spectrin/dystrophin repeat homology <SP13>
R; Yoon, S.H.; Kentros, C.G.; Prchal, J.T.	Query Match 5.7%; Score 315.5; DB 1; Length 2137;		F; 1689-1791/Domain: spectrin/dystrophin repeat homology <SP14>
Gene 91, 297-302, 1990	Best Local Similarity 20.3%; Pred. No. 1e-05;		F; 1792-2007/Domain: spectrin/dystrophin repeat homology <SP15>
A; Title: Identification of an unusual deletion within homologous repeats of human reticul	Matches 197; Conservative 167; Mismatches 328; Indels 277; Gaps 45;		F; 1802-2007/Domain: spectrin/dystrophin repeat homology <SP16>
A; Reference number: JT0554; MUID:91007291; PMID:1976574	Query 285 GRKP-NASOSLLVNUCKEVTRKNGVKTPTTSWRNGSFCATLHHFRDLDIYKLNSPQ 343		F; 2008-2118/Domain: spectrin/dystrophin repeat homology <SP17>
A; Accession: JT0554	Db 169 GRETSKAKDALLWQMKTAGYPHVNNTFSSWKGALFAFLNHKHFDLIDFDKLDS 228		
A; Molecule type: mRNA	Qy 344 DIKENKVKAYD-GFASIGISRLLPSPDMTLLAIPDKLTWMTYQIRAHSGQSLNVPQ 402		
A; Residues: 1334-1373, 'R', 1375-1432; 1909-2137 <WT2>	Db 229 NARKNLHAFNVAEROLGIPLIPLPED-VFTENPDEKSITYVVAFYHFS--RKKVLA 285		
A; Cross-references: UNIPARC:UPI00016A608; GB:J05500	Qy 403 BENSSKSTKGVNEYDTINNSVDOKEFKFIAELSDL-----436		
A; Title: Molecular cloning of the cDNA for human erythrocyte beta-spectrin.	Db 286 B---GKRVGVKDVIAETKMI---EKYGSLASDILTWTQQTIVLNRSKPNLSLQQ 340		
A; Note: authors Yoon et al. show it to be the predominant residue at position 1374 and	Qy 437 -----KRBBLQPIISGAVIDFLSODDSVTFNDVGSEGESEBEHQMPDDHLSPS-- 483		
R; Prchal, J.T.; Morley, B.J.; Yoon, S.H.; Coetzter, T.I.; Palek, J.; Conboy, J.G.; Kan, Y	Db 341 LQAFSTRTVTEKPKFQE---KGNILEV-----LFTIQSRMRANIQKVTPHDGKLVDIN 393		
Proc. Natl. Acad. Sci. U.S.A. 84, 7468-7472, 1987	Qy 484 -----TASPYCRAFTSKDPE---PKQSOSSGRSGSQDPGIGCNTDSTAQAVLQGKRL 534		
A; Reference number: A39885; MUID:88041127; PMID:3478706	Db 394 RAWESLSEAGYRRELALRNBLIROKBLQSLARR-----FDRKAMRETLNENR 443		
A; Accession: A39885	Qy 535 IKAET---LELSDIYVSDGKKSOMSPPFICERTD---EOKLQTL-DIGSNLKEKLENR 586		
A; Molecule type: mRNA	Db 444 LVAGDNFGTDAAVTEAKKCHB----AETDPAVVERVALDEDQELBKENVHYDK 497		
A; Residues: 2105-2137 <WT3>	Qy 587 SLERCSDPSPPIKKSLSPTSKULGYSYRDILAKKKHSRQTESDPADRTLNHADH 646		
A; Cross-references: UNIPARC:UPI0000173DB7; GB:M37885	Db 498 RITARKDNILR-----WSYI-Q---EIQSQRORIETTIALQKLFPQDLHSIDW 543		
A; Molecule type: mRNA	Qy 647 SSKVVOHR-----LQROEELKERAVALBQARRDAIKAGNKHTNTATPF---- 693		
A; Title: Properties of human red cell spectrin heterodimer (side-to-side) assembly and i	Db 544 MDEIKAHLLSAEFGKHLKLVEDLIQKHKLM---EADIAQ-GDKVKVTAATLKFCK 598		
A; Reference number: B42872	Qy 694 ---CNRQL-----SDQDER-----RRROLRERARQL----IARARSGVNUSE 729		
A; Molecule type: protein			
A; Residues: 47-56-293-302; 1837-1846 <SP2>			
A; Cross-references: UNIPARC:UPI0000173DBB; UNIPARC:UPI0000173DB9; UNIPARC:UPI0000173DBA			

Db	599	GYQRCPOVYDQRMSHLEQCPPEELNSMAGARTQI-EQSRLWKFPMWEDBASWIKERK	657	QY
Db	730	LPSGEMALEK----JKERSISGSDENDNTIEDTWEIPE--GFVUGGGDELNLNLEN	780	Db
Db	658	-QIYSSLDYCKDLTSVLILQRKHKPFDLGLDHLBSIQFOEAHGMVA-----RN	707	QY
Db	781	DLFDP--EONSKLUDKLUKULUQPQVANSPSSAAQAVTESSQDMGGTBLARTERL	838	Db
Db	708	ERGHQQBARIKEVSAQWQDQLQKLAFCCKNLQDENPQFGADDLGAWLQD-----	761	QY
Db	839	OKTTERPRNPVUVVKSDSTWTKTOLQSFOSYIENRPFMKGKRSSTQEDTKKGKNECAIMET	898	Db
Db	762	--AHLJSGEDVGQDEGATRALGKHDPL--ELEBSRGWMEHLEO-----QA	806	QY
Db	899	QRKPSDEVALKGKMTSQVYNGLALENEQKOIDTRALVEKRLYLMDFGRANTEBEE	958	Db
Db	807	QGPFFEE-----FRD-SPDVTHRLQALRBLYQGVAQDRLDORLQLRQLDLYWFGTD	858	QY
Db	959	AMMQEFMLVNKKQALTRNNQLSILEKEHDLERYYELNRELQAMATED-----	1009	Db
Db	859	A-CBLW--MGKEKEKWALEMEMPDTLEDIEVORHFDILDQEMKLMTQIDGVNLANSI	914	QY
Qy	1010	-----WO-----KTEAQKRREQL-----	1026	Db
Db	915	VESGHPRSREVVKQYODHLMTRWQAFQTLVSRERKAVDSALRVHTCVDCEETSKWITDKT	974	QY
Qy	1027	-----LVALVNRDLVRLD-----LDAEQKQABE-EDBEHLERTLEQN	1063	Db
Db	975	KVVESTKDPGRDLLAGTIAQORKQSSLERVAATQARVADALERESQLMDSHPSQ--KENI	1032	QY
Qy	1064	GKOMAKKEE 1072	Db	604
Db	1033	GOROKHLEE 1041	QY	692
Db	72940	-----LPSYGENAA-----EKLKERSKASGDDENNTEDNEBEGFV--	768	Db
Db	727	STDTGDRDIVTVSHLAKHNAENNLRDLEYKLDRDVSQKGELQDSDIPSNDNIPPLAET	781	QY
Db	769	-----VGGDELTNLENDLDPPE-----QNSKLVDK	795	Db
Db	782	RDYINKLKLSASRKERLAGGVSYQOFFDADDVRYDYLTRKMSBDVGKDEGTWILL	841	QY
Db	796	LKKLLEVQPVQAN-SPSSAAQAVTESSQDMGKSGTEDLRTERLQKTERFRNPVVFSDK	854	Db
Db	842	LKGHDVVIDELQFDHQTKVLUHAKAESLPOARE-HPDLR-QRLDTK-----	888	QY
Db	855	STWFKTQJOSFSYIENRPFMKGKRSSTQ-----EDTKKGNBKAATMET--OR	900	Db
Db	889	--QKAELENLSO-----LKKQKLIDLASYLYKLYSDADSWSWIDEKGKULATLVR	938	QY
Db	901	KPSDEVALKGKMTSQVYNGLALEN-----EKKOIDTRAL	939	Db
Db	939	DISBEVETMKERFDTLEQDKNRAKAVTWNNDLAROLLUNVEHRNSDDILHRQKLNWARA-	997	QY
Db	940	VEKRLYLMDFGRNTTEEEAMMOEFML-----VNNKKNLR---RMMQSLLEKE	987	Db
Db	998	--QLRDMDQKQEN-ELEAHRLTFRIDCQEVWTMLEDKTRVLEDSLALTUDLNSGVMK-	1052	Qy
Db	998	HDIJERRVSYLLNRELRAMIA-----IDWQKTEAQKREOL-LDDBLVALVNRD	1035	Db
Db	1053	-LQRRLSMRERDGAQKLOSLKHEADDIBERPOERAQARREDIKRIHQWDILNK-	1109	Qy
Db	1036	ALVLDLDAQKQABE-----EDBEHLERTLEQKGMKAKER 1071	Db	1110
Db	1110	--TREHEAKLDEAGDLQFLRLDHFQWLTATQRQVASEER 1149	Result 13	
T8296	289	NASQSLUWCKEVTKTKYKVKTINFTTSWRNGLSPCALLHHFRPDLIYKSINPQDKEK	348	C;Species: Entamoeba histolytica
Db	229	SAXEALLWQCMQTKAGYENUNVKNSTSWRDGLAFNALJHKRPDLVYDQKNSNALYN	288	C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Qy	349	NKCGAYDGFAAS-IGTSRLLRPSDMVTLA1PDQLTWMTYXQIRAHFS-----GQELNV	399	C;Accession: T18296
Db	289	:-----MINYETUSSDILMENTAKTQOLMLERHFNENLREGVQRO-----LT	347	R;Guillen, N.
Db	400	V--QIRENSSSKSTYKVGVYETPDTNSVSD-----QEKFYAEALSQKREBELQQPI	447	submitted to the EMBL Data Library, February 1997
Qy	348	VNBMLMENDK-----MINYETUSSDILMENTAKTQOLMLERHFNENLREGVQRO-----LT	397	A;Reference number: Z18865
Db	348	LOSADFDTAENQGLAKFELDAED-VNDQDPEKESITTYVYHIFNKUKQDN1QGKRIGK	347	A;Accession: T18296
Db	348	VNBMLMENDK-----MINYETUSSDILMENTAKTQOLMLERHFNENLREGVQRO-----LT	397	A;Status: Preliminary; translated from GB/EMBL/DDBJ
Db	348	-----MINYETUSSDILMENTAKTQOLMLERHFNENLREGVQRO-----LT	397	A;Molecule type: DNA
Db	348	-----MINYETUSSDILMENTAKTQOLMLERHFNENLREGVQRO-----LT	397	A;Residues: 1-2139 <GUT>
Db	348	-----MINYETUSSDILMENTAKTQOLMLERHFNENLREGVQRO-----LT	397	A;Cross-references: UNIPROT:Q07569; UNIPARC:UPI00000802D3; EMBL:L03534; NID:g1850912; PIR:
Db	348	-----MINYETUSSDILMENTAKTQOLMLERHFNENLREGVQRO-----LT	397	C;Genetics:

A;Gene: mhca  
C;Superfamily: myosin heavy chain; myosin motor domain homology  
P;91-780/Domain: myosin motor domain homology <MMO>

Query Match 5.4%; Score 299; DB 2; Length 2139;  
Best Local Similarity 20.2%; Pre. No. 5.2e-05;  
Matches 254; Conservative 213; Mismatches 448; Indels 340; Gaps 53;

Qy 38 PLREGKATDBEMOSL-----ASLVSMSKQADIGCNLDPEEDEHDDENRVNQ 83  
Db 859 PEEBEGKKKDKIEDLKKKLABEIKKREAAENALASATAKTEGELEAKIQDLED-----  
Qy 84 EERAAKAKITELINKINF--LDEARKDLATVNSNPDPDAEL----NPFCD-----  
Db 911 -----KISELSLSAABEQLDQBLNLKJENL---EDKDEBLKETIDNLKDKLDSKLKG 961  
Qy 129 PDSEBRSPITETASPRKTEDSFNNNSTNPKEYQTPOVLNPFRDEPEAKT-----I 177  
Db 962 EDLEVITEILNSQINTLNATWDKOKTIAEQ-----ESIDEKEBTIKGDIKLLEE 1016  
Qy 178 KDSPPOSTKRKNIRPVDMSKLYA-----DSKTRBEELEDSENPNPFTEPKSTPPN 227  
Db 1017 RDDLEQDRADVSATKODIAKLINKLTIEBEDAKDSEIAKQBLEDEN-----KKN 1067  
Qy 228 NLVNVQEL---TERRVKAAPPVULSPKTVNLNEVTSAGKDLSTSPKSPIPSP 282  
Db 1068 DLNTLILQOTOLKLGTEKSLAQVAQATKKKASDERDTLQN----- 1107  
Qy 283 VLGRKPNASGSSLLVNCKEVTRVYRGKVTINFTSWRNGLSSFCALIHFRPDLDYKSLNP 342  
Db 1108 -LENVKLTITLTKTAKDALKISIK-----QDYEDL----- 1139  
Qy 343 QDIKENKKKAVDGAFASIGRSLRPLSDMVLIAIPDQLT---WMTLYQIRAHPSQ--- 395  
Db 1140 ---BDDKNKIEGD-----LRAQRKKIKELDDBITKGADVSQYLOQKORKEYESQAK 1187  
Qy 396 ---ELNVHQFERNSSKTYKGNYETD-NSSVQDKFVYELSDQKREPBLOQPIGAVD 451  
Db 1188 MQEKKAEIGNVNDKNTCTIKEKBLTOSLQEKLDTEVEKDAD-KKKKEIEKMKAL-- 1244  
Qy 452 FLSQDSVSFVINDSGYGBSSEHQTPDHLSFS-----TASPCCRRTS-DTERQKSQ 503  
Db 1245 ---QBEKENV-ESSNISTECKKKLENDNICKQKLDMDWADNECLKAKAKDLEAQLEW 1300  
Qy 504 SSGRTSGSDPREGICNTSDSTAQVQLGKRLKAAETLELSDLYWSDKKDMSPRFICET 563  
Db 1301 ODNHKAVADABELLNKKKAGSDKELNSLKAELAALTAKSVVESKNDSENEKALSEEI 1360  
Qy 564 DRQKQTLGDSNEKEKLENSRSIACRSRSPBSPK---TLSPTSKUGYSYRDL--- 618  
Db 1361 DOANBKLNNTQDADLKATADQEOANTEKKEAVTAORDKLVADNKONTKTBEKARDE 1420  
Qy 619 -----LAKKXHASLRQTESFPADRTLNHADHSISKVQHRLLSROEELK---ERA 666  
Db 1421 YKVENEYEVKVKRKAIDERANENDIKKORMANKEKQVKVKELEGKETKDNNAECD 1480  
Qy 667 RVLLEQARRDALKAGNK---HNTNTATPFCNROLS---DODDEERRRQFERA--- 714  
Db 1481 SIFTAKQSDADBELNLTVEBHDDEVVK---LNTQITKUJRDNGSABEELNELRSKADKO 1538  
Qy 715 RQIARLEARQVTKMSLPSGYGMAEK-----LKERSKASDENDNIRDNE- 761  
Db 1539 KKXSELEBQVNELESRPVGTGNADENBTKRDAQIADNPKALMKGVQNONQATNKEI 1598  
Qy 762 -----EIPRGFVWGGDELNLNLENDLDPTEONS-----KLVDLKL 796  
Db 1599 KAKNDLITSKRTE-----NEMKLEKAKKQLEQDKDADGAVSECTIKRKGLEEV 1651  
Qy 797 KKL-LRVOP---QVANSPSSAAQAVTBESSBDMKGSGTRDLRTERL-----OKTTER 844  
Db 1652 KKLTTBQIAALKFQI-NAPSSVAQEBKORLSDIAKLKQLEORTTAANAEEKKLQIA 1710  
Qy 845 FRNPVWTF-SKSTVTKTQLOSPSQVIENTPMPKRSIQBDTKGNGNEEKAITQKPS 903

RESULT 14  
S28916  
dystrophin - mouse  
N;Alternate names: duchenne muscular dystrophy protein  
C;Species: Mus musculus (house mouse)  
C;Accession: 22-Nov-1993 #sequence revision 03-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S28916; B07162; S10922; C43837; B0134  
R;Blas, R.D.; Phelps, S.F.; Correra, M.D.; Roberts, R.; Caskey, C.T.; Chamberlain, J.S.  
Nucleic Acids Res. 1992, 20, 1725-1731, 1992  
A;Residues: Human and murine dystrophin mRNA transcripts are differentially expressed during development. Reference number: S28916; PMID:92253376; PMID:1579466  
A;Accession: S28916; MUID:92253376; PMID:1579466  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-3678 <B1E>  
A;Cross-references: UNIPARC:UPI0000027987; EMBL:M68859  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
R;Koenig, M.; Hoffman, B.P.; Bertelson, C.J.; Monaco, A.P.; Feener, C.; Runkel, L.M.  
Cell 50, 50-517, 1987  
A;Title: Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and preliminary analysis. Reference number: A90897; MUID:87273512; PMID:3607877  
A;Accession: B17162  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-201 <KOB>  
A;Cross references: UNIPARC:UPI0000177686  
R;Nudel, U.; Zuk, D.; Binat, P.; Zeelon, B.; Levy, Z.; Neuman, S.; Yaffe, D.  
Nature 337, 76-78, 1989  
A;Title: Duchenne muscular dystrophy gene product is not identical in muscle and brain. Reference number: S06461; MUID:89082658; PMID:2909892  
A;Accession: S10922  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-106 <NUD>  
A;Cross references: UNIPARC:UPI0000177687; EMBL:X14183  
R;Rapaport, D.; Leiderman, D.; den Dunnen, J.T.; Grootenhuis, P.M.; Van Ommen, G.J.; Pijnacker, D.; Differentiation 49, 187-193, 1992  
A;Title: Characterization and cell type distribution of a novel, major transcript of the A;Reference number: A3837; MUID:92316332; PMID:1377655  
A;Accession: A3837  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: MREHKG'3069-3181 <RAP>  
A;Cross references: UNIPARC:UPI0000177688  
A;Note: sequence extracted from NCBI backbone  
A;Reference number: A0134; MUID:88018015; PMID:3659917  
A;Accession: B0134  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 300-676, 'P', 678-1390 <HOP>

A-Cross-references: UNIPARC:UPI0000177589; GB:MI18025  
 C-GeneID: 11/1  
 A:Introns: 11/1  
 A:Note: the list of introns may be incomplete or incomplete binding domain homology; spectrin/dystrophin repeat homology <SP1>  
 C:Superfamily: dytrophin; alpha-actinin actin-binding domain homology  
 C:Keywords: actin-binding; alternative splicing  
 F:14-233/Domain: alpha-actinin actin-binding domain homology <ACT>  
 F:340-449/Domain: spectrin/dystrophin repeat homology <SP1>  
 F:450-558/Domain: spectrin/dystrophin repeat homology <SP2>  
 F:279-324/Domain: spectrin/dystrophin repeat homology <SP3>  
 F:304-8-3085/Domain: WW repeat homology <WW1>

Query Match Best Local Similarity 5.4%; Score 297.5; DB 2; Length 3678; Matches 209; Conservative 20.2%; Pred. No. 0.00012; Mismatches 348; Indels 307; Gaps 46;

QY 186 KRKKIRPVDMVKVLYADSSKTEELDESNPPFYR-----PKSTPPP 226  
 Db 12 REREVQKCTFTKMINAQPSKFGKPHD--NLFLQLQGRKLLEGITQKUPKE--KG 67

QY 227 NLNVNPVQOLETERVRVKRKAAPPVPLSPKPGVLNEN-----TV 264  
 Db 68 STRVHALNNVNKAHLRVLQKGNVLNVNIGSTDIVGHNHKTGLIWNIIHWQVKNVKTI 127

QY 265 SAGKDLSTSPKPSLPSVPLSPVUGRKENASQSLIVWCKEVTKYRGKMTTSWRNGLSFC 324  
 Db 128 MAGL-----QQTNEKILLSWVQSTNRYPQVNINTTSWRNGLSFC 170

QY 325 ALILHHFRPDLLDYKSLNPO-DIKENNKGAYD-GPASIGSRLEPSDMALLPDKLTW 382  
 Db 171 ALHSHRPDLFDMNSVPSHATORLEAFNAKQGLIEKLDPED-VATTYPDKSIL 229

QY 383 TY--LYQTRAHFSGQELNVWQEBENSSKSTYKVGNYETDTNSVQDKRPFYABLSDKE 439  
 Db 230 MYTSLRFQVLP-----QOVSIAQOEVEMPLR-----TSSKVTRBHF---OLHQ 272

QY 440 PELQQPISGAVADELSQDSDSVFVNDGQVESESEHQTDPDHS-----TASPCCR 491  
 Db 273 MHYSQQT-----VSLAQGYBOTSS---SPKPRFKSYAFTQAOVAT 311

QY 492 TKSDTBEPQKSQOSGSGRTCSDDPQICS---NTYSTQAQV-----LLGKRULKAETL 542  
 Db 312 SOSTQSPPSQHLEAPRKSKSLDSLMETEFLVNLQSYQTALEBEVLSWLSAEDTURAQBS 371

QY 543 SOKVSDKKDDMSPPFICBETDQKL--OTLDIGSNL-----BREKELNS 585  
 Db 372 NDPEBVKEQPHAHGFMMDLTHOSHGLGVNLQGQSLVKGKLSSEDERAEVWQMNLLNS 431

QY 586 RSLECRCSUPPESPIKTSLSUPTSKLGYSRSRDLQAKKHAS--LRQTES-----D 633  
 Db 432 R\_WEC-----LKVASMVKQSKL-HKVLMDLQNKUKLBEDMLTKYBERTKMEERPPG 482

QY 634 PDADETTLNHDHSKIVHRLLSRQEELKERARVLEQARDAAKAGKNTINTATPF 693  
 Db 483 PDLR-----DLKCQVQOHKVL---QEDLQQ-----EQVR-----VNSLTHM 515

QY 694 CIRQLSDQOQDERRRQLRERAROLIAEARSGVNSNSELSPYGMMAEKUKERKASGBEND 753  
 Db 516 V-----VVDE-----SSGHATAALBEQJKVLGDRW 543

QY 754 NI-----EDITNER-1PEGFVNGSGDELTLNEDL--LDPPEONKL- 791  
 Db 544 NTCRWTEDRWIVLQDILKWHFTBEOCLFLSTWLSEKEADAMKNIQTSGFKDNEMMSSHL 603

QY 792 -----VDLKUQKCLEVOPQVANSP- SSAQKAVTSESEQMKSGT--DIRTERIQT 841  
 Db 604 KISTKLIDLEKQPTMEBLKLSSINODLISALKNKSUTOMENINENPAQRWDNLQLEKS 663

QY 842 TSPRNPVVFSPKQSTVTKQQLQSPSQYIENR-----DEMKRORSIQDTPK 886  
 Db 664 SAQISQAVTTQPSLQTQTVMETWMTREQIMWKHAQBELEPPPPQKQKQGQITVDSLR 723

QY 887 KSENEKAALTETQRKPSBEDEVINKGKFQTSQVW---GELAALENBQKQDITRAALVEK 942

RESULT 15  
 JCS837  
 36K Golgi complex-associated protein - rat  
 CSpecies: Rattus norvegicus (Norway rat)  
 CAccession: JCS837  
 CRole: C.; Fujiwara, T.; Sohda, M.; Hong, H.S.; Misumi, Y.; Ikebara, Y.  
 R;Ioki, C.;  
 Cell Struct. Funct. 22, 565-577, 1997  
 A-Title: Identification and characterization of rat 364-kDa Golgi-associated protein recr  
 A-Reference number: JCS837; MUID:98093490; PMID:9431462  
 A-Status: nucleic acid sequence not shown  
 A-Molecule type: mRNA  
 A-Residues: 1-3187  
 A-Cross-references: UNIPROT:Q63714; UNIPARC:UPI000008886; DDBJ:225543; NID:9516825; PID:  
 C-Comment: This protein plays a role in the formation and maintenance of the characteristic  
 F:49-539, 624-1176, 1238-1707, 1763-3114/Domain: coiled-coil leucine zipper #status predicted  
 F:3165-3187/Domain: membrane anchor #status predicted <MDA>  

Query Match Best Local Similarity 5.4%; Score 297; DB 2; Length 3187; Matches 241; Conservative 20.1%; Pred. No. 0.0001; Mismatches 44; Indels 312; Gaps 52;

QY 51 SLASLVSVKQADIGNLDDFEEDNBDDDENRVQBEKAKI---TELINKLNPLD---B 102  
 Db 1010 SLRUTISBEKEVEL-----EGIRDRDIKEKAALEEQLQVQRMQTDQIQLQKQDILQER 1063

QY 103 ASKDQLATVNSNPRFDPPDABLNPFQGDPDSESPRITETASPRKNTDSPFVNNSYNPFKEVOTP 162  
 Db 1064 ITENQATIOKFITGTMDA-----GDGDSAVKETSVPSSPRAGGER----- 1104

QY 163 QVLNPPDEPEARTVKISSQPPQSTK-RKTRPVDMVKLYADSSKTE---EELDSNPF 217  
 Db 1105 -----WPKPELGKIVDLEKLEKTCQKQKQLOALISLISKIAKQKQKQKHLKQELBQDKA 1158

QY 218 YE-----PKSTPPPNLNLVNPVQBLEFERRVKRKAAPPVPLSP--KTVGLMENTSGK 268  
 Db 1159 YHQLQBGDFQSKKENENIRAPRQLQKESTDQQLGQGQEPHTGSEGSLQEGTPASE 1218

QY 269 DUSTSPRSPSPSPVPLSPVUGRKENASQSLIVWCK--EVTRKNGVKGKTNFTSWRNGLSFC 325  
 Db 1219 SDLHAQSFHPGTATQATVSAQ-IQDQLKEIEVEKEELKLSSSTSE----- 1268

QY 326 ILMHFREDLIDYKSLNPDQKIDENKNGKAYDGFASIGSRL--LEPSDMVLAIPDKLTW 382  
 Db 1269 LTKKSBELLQBLQBOQINEGGLIONLKAHSHEAKHTBQKLBRSQQLKIALDEHLKTLQ 1328

QY 383 TLYQIRAHFSGQ-----LNUVQIBBNSSKSTYKVGNYETDTNSVSD 426  
 Db 1329 PELETQKHVGQKEEVSYVLYQQLGKETQTLTQEMESEGERLVALHTOLEMQKEHE 1388

QY 427 EK-----YAELESLDKRER-----ELQOQPISGAVDELSQDJSVFFVNDGQVGESESE 472  
 Db 1389 ERLQKVQEICBLKKQPKELERESKAKQQLQKQQL--ISRKEALKENK-SLQQLSS 1445

QY 473 HQTDDHLSPTASPICRTKSDTEPKQSQSSGRTSGSDPGCISNTSTDQAVQVLLGKK 532



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